

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 29, 2004, 10:34:37 ; Search time 46 Seconds  
(without alignments)  
1800.267 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 1349

Sequence: 1 MKPTTISLLQKYKDKKRFA.....ROYMAEVESGVVPEBHSFH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349	100.0	264	12	US-09-820-745-7
2	1345	99.7	264	9	US-09-815-242-10038
3	1345	99.7	264	12	US-10-282-122A-56418
4	1243.5	92.2	264	12	US-10-282-122A-56418
5	1237.5	91.7	269	9	US-09-815-242-13902
6	1231.5	91.3	263	12	US-10-282-122A-56060
7	1204.5	89.3	263	9	US-09-815-242-11707
8	1204.5	89.3	263	12	US-10-282-122A-50170
9	1074	79.6	263	12	US-10-282-122A-73508
10	1063.5	78.8	266	12	US-10-282-122A-77867
11	968.5	71.8	263	12	US-10-282-122A-68789
12	950	70.4	264	12	US-10-282-122A-77094
13	923.5	68.5	267	12	US-09-820-745-8
14	795.5	59.0	280	12	US-10-282-122A-68084
15	745.5	55.3	266	12	US-10-282-122A-69916

16	726	53.8	263	12	US-10-282-122A-65862	Sequence 65862, A
17	726	53.8	269	12	US-10-282-122A-45216	Sequence 45216, A
18	723	53.6	263	12	US-10-282-122A-65261	Sequence 65261, A
19	719	53.3	271	12	US-10-282-122A-49327	Sequence 49327, A
20	713	52.9	271	12	US-10-282-122A-47835	Sequence 47835, A
21	709	52.6	271	12	US-10-282-122A-50718	Sequence 50718, A
22	689	51.1	280	12	US-10-282-122A-63067	Sequence 63067, A
23	685.5	50.8	266	9	US-09-815-242-12047	Sequence 12047, A
24	685.5	50.8	266	12	US-10-282-122A-66716	Sequence 66716, A
25	610	45.2	275	12	US-10-282-122A-52931	Sequence 52931, A
26	604	44.8	275	12	US-10-282-122A-52540	Sequence 52540, A
27	601	44.6	279	12	US-10-282-122A-45673	Sequence 45673, A
28	598.5	44.4	275	9	US-09-815-242-10842	Sequence 10842, A
29	598.5	44.4	275	12	US-10-282-122A-56941	Sequence 56941, A
30	598.5	44.4	275	12	US-10-282-122A-57608	Sequence 57608, A
31	588.5	43.6	281	12	US-10-282-122A-62753	Sequence 62753, A
32	588.5	43.6	281	12	US-10-282-122A-64679	Sequence 64679, A
33	579.5	43.0	276	12	US-10-282-122A-51930	Sequence 51930, A
34	576.5	42.7	284	12	US-10-282-122A-61944	Sequence 61944, A
35	565.5	41.9	274	12	US-10-282-122A-54276	Sequence 54276, A
36	565.5	41.3	286	12	US-10-282-122A-63901	Sequence 63901, A
37	547.5	40.6	287	14	US-10-156-761-13470	Sequence 13470, A
38	546	40.5	277	12	US-10-282-122A-60709	Sequence 60709, A
39	527.5	39.1	271	9	US-09-738-626-3633	Sequence 3633, Ap
40	526.5	39.0	272	12	US-10-282-122A-44309	Sequence 44309, A
41	522.5	38.7	272	12	US-10-282-122A-70825	Sequence 70825, A
42	520.5	38.6	261	9	US-09-815-242-5828	Sequence 5828, Ap
43	520.5	38.6	274	8	US-08-781-986A-5243	Sequence 5243, Ap
44	520.5	38.6	274	12	US-10-329-624-5243	Sequence 5243, Ap
45	511.5	37.9	263	9	US-09-815-242-12662	Sequence 12662, A

ALIGNMENTS

RESULT 1

US-09-820-745-7  
; Sequence 7, Application US/09820745  
; Publication No. US20040053385A1  
; GENERAL INFORMATION:  
; APPLICANT: Blundell, Tom L  
; APPLICANT: Abell, Christopher  
; APPLICANT: Inoue, Tsuyoshi  
; APPLICANT: von Delft, Frank  
; TITLE OF INVENTION: Crystal Structure  
; FILE REFERENCE: 620-139  
; CURRENT APPLICATION NUMBER: US/09/820,745  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
; US-09-820-745-7

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Best Local Similarity	100.0%	Pred No.	4	2e-134			
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Gaps	0						
Qy	1	MKPTTISLLQKYKDKKR	FATITAYDYSFAKLFAD	EGLNMLVGD	SLGTMVQGH	STLPLV	60
Db	1	MKPTTISLLQKYKDKKR	FATITAYDYSFAKLFAD	EGLNMLVGD	SLGTMVQGH	STLPLV	60
Qy	61	TVADIAVHTAAVRGAPN	CLLLADLPFMAYATPEQAF	ENAAVTMRAGAN	NVKEGEMLV	120	
Db	61	TVADIAVHTAAVRGAPN	CLLLADLPFMAYATPEQAF	ENAAVTMRAGAN	NVKEGEMLV	120	
Qy	121	ETVQMLTERAVPVCGH	GLTTPQSVNIFGGYKQV	GRGDEAGDQL	SLDALALEAAG	QLLV	180
Db	121	ETVQMLTERAVPVCGH	GLTTPQSVNIFGGYKQV	GRGDEAGDQL	SLDALALEAAG	QLLV	180
Qy	181	ECVPVELAKRIT	EALAIPIVIGAGNV	TGQILVMDAF	IGTGGHIPKFN	FLAETGDI	240

Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVQYMAEVESGVYPGEEHSPH 264  
 Db 241 RAAVQYMAEVESGVYPGEEHSPH 264

RESULT 2

US-09-815-242-10038  
 ; Sequence 10038, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; TITLE OF INVENTION: Prokaryotes  
 ; FILE REFERENCE: ELITRA-011A  
 ; CURRENT APPLICATION NUMBER: US/09/815,242  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 14110  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 10038  
 ; LENGTH: 264  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 US-09-815-242-10038

Query Match 99.7%; Score 1345; DB 9; Length 264;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-133;  
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MKPTTISLLQKYQDKKRFAITATAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60  
 QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMEAGANVMKIEGGEWLV 120  
 Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMEAGANVMKIEGGEWLV 120  
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 Db 121 ETVQMLTERAVPCVCHGLTTPQSVNIFGGYKVGQRDEAGDQLLSDALALEAAGALLVL 180  
 QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVQYMAEVESGVYPGEEHSPH 264  
 Db 241 RAAVQYMAEVESGVYPGEEHSPH 264

RESULT 3

US-10-282-122A-56418  
 ; Sequence 56418, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA-034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 56418  
 ; LENGTH: 264  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 US-10-282-122A-56418

Query Match 99.7%; Score 1345; DB 12; Length 264;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-133;  
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKPTTISLLQKYQDKKRFAITATAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60  
 Db 1 MKPTTISLLQKYQDKKRFAITATAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60  
 QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMEAGANVMKIEGGEWLV 120  
 Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMEAGANVMKIEGGEWLV 120  
 QY 121 ETVQMLTERAVPCVCHGLTTPQSVNIFGGYKVGQRDEAGDQLLSDALALEAAGALLVL 180  
 Db 121 ETVQMLTERAVPCVCHGLTTPQSVNIFGGYKVGQRDEAGDQLLSDALALEAAGALLVL 180  
 QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVQYMAEVESGVYPGEEHSPH 264  
 Db 241 RAAVQYMAEVESGVYPGEEHSPH 264

## RESULT 4

JS-10-282-122A-76055  
; Sequence 76055, Application US/10282122A  
; Publication No. US20040029129A1

## GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

## TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 76055

; LENGTH: 264

; TYPE: PRT

; ORGANISM: Salmonella typhi

JS-10-282-122A-76055

Query Match 92.2%; Score 1243.5; DB 12; Length 264;

Best Local Similarity 91.6%; Pred. No. 6.2e-123;

Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

2Y 2 KPTTISLLQKVKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 61

2b 3 KPTTIAVLQCKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 62

2Y 62 VADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAIVNRAGANVMVKIEGGSWLVE 121

2b 63 VEDIAVHTAVRRGAPNCLLLSDLPFMAYATPQAFENAAIVNRAGANVMVKIEGGAWLVD 122

2Y 122 TVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGAQLLVLE 181

2b 123 TVKMLTERAVPVCGHLGLTPQSVNIFGGYKIQGRGD-AGQILLDDALAEAGAQLLVLE 181

2Y 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIIPKFAKNFLAETGDIR 241

2b 182 CVPVELAKRVTTEALSIPVIGAGNVTGQILVMHDAFGITGCHIIPKFAKNFLAEGDNR 241

2Y 242 AAVRQYMAEVESGYYPGEHSFH 264

Db 242 AAVRQYMAEVESGYYPGEHSFH 264

## RESULT 5

US-09-815-342-13902

; Sequence 13902, Application US/09815242

; Patent No. US20020061569A1

## GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

## TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13902

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Salmonella typhi

; NAME/KEY: VARIANT

; LOCATION: (1)...(269)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-815-342-13902

Query Match 91.7%; Score 1237.5; DB 9; Length 269;

Best Local Similarity 91.3%; Pred. No. 2.7e-122;

Matches 240; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

QY 2 KPTTISLLQKVKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 61

Db 8 KPTTIAVLQCKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 67

QY 62 VADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAIVNRAGANVMVKIEGGSWLVE 121

Db 68 VEDIAVHTAVRRGAPNCLLLSDLPFMAYATPQAFENAAIVNRAGANVMVKIEGGAWLVD 127

QY 122 TVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGAQLLVLE 181

Db 128 TVKMLTERAVPVCGHLGLTPQSVNIFGGYKIQGRGD-AGQILLDDALAEAGAQLLVLE 186

QY 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIIPKFAKNFLAETGDIR 241

Db 187 CVPVELAKRVTTEALSIPVIGAGNVTGQILVMHDAFGITGCHIIPKFAKNFLAEGDNR 246

QY 242 AAVRQYMAEVESGYYPGEHSFH 264

Db 247 AAVRQYMAEVESGYYPGEHSFH 269

```

RESULT 6
US-10-282-122A-56060
; Sequence 56060, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56060
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-56060

Query Match          91.3%; Score 1231.5; DB 12; Length 263;
Best Local Similarity 91.3%; Pred. No. 1.1e-121;
Matches 241; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

Qy      1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60
Db      1 MKPTTISLLQCKQEKRFATITAYDYSFAKLFAEGLNVLVGLDGLMTVQGHDSLTPV 60

Qy      61 TVADIAYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAATVMRAGANMVKIEGGEWLV 120
Db      61 TVEDIAYHTRAVRGAPNCLLLADLPFMAYATPEQTANAAIWMRAGANMVKIEGGAWLA 120

Qy      121 ETVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDSALALEAAGAQLLVL 180
Db      121 DTVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDSALALEAAGAQLLVL 179

Qy      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
Db      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 239

Qy      241 RAAVQYMAEVESGVYPGEHSFH 264
Db      240 RAAVQYIADVESGVYPGEHSFH 263

```

```

RESULT 7
US-09-815-242-11707
; Sequence 11707, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11707
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-815-242-11707

Query Match          89.3%; Score 1204.5; DB 9; Length 263;
Best Local Similarity 89.0%; Pred. No. 8.2e-119;
Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy      1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60
Db      1 MKPTTIALQCKQEKRFATITAYDHSFAKLFADEGINVLVGLDGLMTVQGHDSLTPV 60

Qy      61 TVADIAYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAATVMRAGANMVKIEGGEWLV 120
Db      61 TVEDIAYHTRAVRGAPNCLLLADLPFMAYATPEQTANAAIWMRAGANMVKIEGGAWLA 120

Qy      121 ETVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDSALALEAAGAQLLVL 180
Db      121 DTVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDSALALEAAGAQLLVL 179

Qy      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
Db      180 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 239

Qy      241 RAAVQYMAEVESGVYPGEHSFH 264
Db      240 RAAVQYIAEVESGVYPGEHSFH 263

```

```

RESULT 8
US-10-282-122A-60170
; Sequence 60170, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu

```

APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 60170

LENGTH: 263

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-10-282-122A-60170

Query Match 89.3%; Score 1204.5; DB 12; Length 263;

Best Local Similarity 89.0%; Pred. No. 8.2e-119;

Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

1 MKPTTISLLQKYKDKKRFATITAYDYSFAKLFADEGLNMLVGDGLGHTVQGHSTLTPV 60

1 MKPTTIALLOKCKQKQKRFATITAYDHSFAKLFADEGINVLLVGDGLGHTVQGHSTLTPV 60

61 TVADIAVHTAAVRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKEGGELV 120

61 TVEDIAVHTAVRAGAPNCLLLADLPMAVATPEQTFANAAVVRAGANNVKEGGAWLA 120

121 ETVQMLTERAVPVCGHGLTTPQSNVIFGGYKVGGRGDEAGDQLLSDALAEAGQLLVL 180

121 DTVRMLAERAVPVCGHGLTTPQSNVIFGGYKVGGRGDEAGDQLLSDALAEAGQLLVL 179

181 ECVPELAKRITETALATPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 240

180 ECVPELAKRITDALTIPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 239

241 RAAVRQYMAEVESGYVPEEHSFH 264

240 RAAVRQYIAEVESGYVPEEHSFH 263

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
 APPLICANT: Zamudio, Carlos  
 APPLICANT: Malone, Cheryl  
 APPLICANT: Haselbeck, Robert  
 APPLICANT: Ohlsen, Kari  
 APPLICANT: Zyskind, Judith  
 APPLICANT: Wall, Daniel  
 APPLICANT: Trawick, John  
 APPLICANT: Carr, Grant  
 APPLICANT: Yamamoto, Robert  
 APPLICANT: Forsyth, R.  
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 73508

LENGTH: 263

TYPE: PRT

ORGANISM: Salmonella paratyphi A

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (72)..(72)

OTHER INFORMATION: X=any amino acid

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (139)..(139)

OTHER INFORMATION: X=any amino acid

US-10-282-122A-73508

Query Match 79.6%; Score 1074; DB 12; Length 263;

Best Local Similarity 81.4%; Pred. No. 5.4e-105;

Matches 215; Conservative 13; Mismatches 34; Indels 2; Gaps 2;

1 MKPTTISLLQKYKDKKRFATITAYDYSFAKLFADEGLNMLVGDGLGHTVQGHSTLTPV 60

2 MKPTTISLLQCKQKQKRFATITAYDYSFAKLFADEGINVLLVGDGLGHTVQGHSTLTPV 60

61 TVADIAVHTAAVRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKEGGELV 120

61 TVEDIAVHTLXTRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKEGGELV 120

121 ETVQMLTERAVPVCGHGLTTPQSNVIFGGYKVGGRGDEAGDQLLSDALAEAGQLLVL 180

121 DTVKMLTERACRFGHGLTTPQSNVIFGGYKVGGRGDEAGDQLLSDALAEAGQLLVL 179

181 ECVPELAKRITETALATPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 240

180 ECVPELAKRITETALATPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 239

RESULT 9

US-10-282-122A-73508

; Sequence 73508, Application US/10282122A

; Publication No. US20040029129A1



181 ECVPELAKRITAEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKPAKNFLAETGDI 240  
181 ECVFVSAKTITGSLNIPVIGAGNVTDGQILVMDHLLGLT-PNAPKFSKNFLOEAGSL 239  
241 RAAVROYMAEVESGVYPGEHSHF 264  
240 PEAVRLVQOQVEQKLPQEQHSHN 263

RESULT 12

US-10-282-122A-77094

Sequence 77094, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zvekind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 77094

LENGTH: 264

TYPE: PRT

ORGANISM: Vibrio cholerae

US-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 68.7%; Pred. No. 7.2e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

1 MKPTTISLQKYKQDKRFRATITAYDYSFAKLPADEGLNMLVGDLSGMTVQGHSTLPLV 60

1 MKKITINDLMKWQEGRKATATAYDASPAQLPESQEMPVLLVGDLSGLMVLQGETDTLPLV 60

61 TVADIAVHTAAVERGAPNCILLADLPMAVATPEQAFENAAATVWRAGANMVKIEGEMVLV 120

61 TVDDIAVHTCRVKGSPNCILLADMPFMSATPEQACENAAKLVRAGANMVKIEGEMVLV 120

121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGQLVL 180

121 DTVMLETERAVPVCAHLGLTPQSVNIFGGYKVGQRGDEQKADKEMVEDALALQERAGQIVLL 180  
181 ECVPELAKRITAEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKPAKNFLAETGDI 240  
181 ECVFAELANRITQILDVPVIGAGNVTDGQILVMDHMFGISANTMPKFSKNFLAETGDI 240  
241 RAAVROYMAEVESGVYPGEHSHF 262  
241 RQAVAKIIEVDVAGAPFDLAHT 262

RESULT 13

US-09-820-745-8

Sequence 8, Application US/09820745

Publication No. US20040053385A1

GENERAL INFORMATION:

APPLICANT: Blundell, Tom L

APPLICANT: Abell, Christopher

APPLICANT: Inoue, Tsuyoshi

APPLICANT: von Delft, Frank

TITLE OF INVENTION: Crystall Structure

FILE REFERENCE: 620-139

CURRENT APPLICATION NUMBER: US/09/820,745

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 267

TYPE: PRT

ORGANISM: Schizosaccharomyces pombe

US-09-820-745-8

Query Match 68.5%; Score 923.5; DB 12; Length 267;

Best Local Similarity 68.2%; Pred. No. 4.7e-89;

Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;

1 MKPTTISLQKYKQDKRFRATITAYDYSFAKLPADEGLNMLVGDLSGMTVQGHSTLPLV 60

3 LKQITITSLRQWKLANKKFCATAYDASFSRLFAEQGMPVLMVGDLSGLMTAQGHSTLPLV 62

61 TVADIAVHTAAVERGAPNCILLADLPMAVATPEQAFENAAATVWRAGANMVKIE-GGEWL 119

63 SVEDIAVHTKSVRGAPNRLMLADLPFMSYSTWEDACKNAAATVWRAGANIVKIEGGNWI 122

120 VETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGQLLV 179

123 FEIVQRLTERSVPVAGHLGLTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGQLLV 182

180 LECVPVELAKRITAEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKPAKNFLAETGD 239

183 LECIPESLABQITKTISIPITIGAGKHTDQQLVMDALGITGRPPKPAKNFLSGAGD 242

240 IRAAVROYMAEVESGVYPGEHSHF 263

243 IRTAIQRYIIVEEQGLYPAEHSHF 266

RESULT 14

US-10-282-122A-68084

Sequence 68084, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zvekind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

```

; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68084
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; US-10-282-122A-68084

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Query Match      59.0%; Score 795.5; DB 12; Length 280;
Best Local Similarity 56.8%; Pred. No. 1.8e-75;
Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;

QY 1 MKPTTISLLQKYKQDKKRFATITAYDSFAKLPADEGLNVLVGDLSGMTVQGHDSLPV 60
Db 15 MEVTLTTUNGKAKGEKITMLTCYDATFAKASQAGVEVLVGDLSGMTVQGHDSLPV 74
QY 61 TVADIAYHTAAVRGAPNCLLIADLPFMAVATPEQAFENAAATVVRAGANVVKIEGSEWLV 120
Db 75 TTAEMAYHTASVYKRGNDGALLITDLPFWAHATPEQAFANSATLWQAGAHVVKIEGAWLA 134
QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAQAQLLV 180
Db 135 ETIRLLAERGVPCAHMGLTPQTNNVLGGYKVGQGRDEAQAQRMRADAIALEQAQAAMLL 194
QY 181 ECVPELAKRITERALATPVIGAGNVTGQILVWHDFAFGIT-GGHIKPKAKNPLAETGD 239
Db 195 ECVPELAAEINAVGIPVIGAGSATDGGVLVLDMLGLSLSGRVPKFKVFMQGPDP 254
QY 240 IRAAVRQYMAEVESGVYFGEHSF 263
Db 255 IHSALVAYVEAVKQVSFFGSEHGF 278

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RESULT 15
US-10-282-122A-69916
; Sequence 69916, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John

```

```

; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69916
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
; US-10-282-122A-69916

```

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Query Match      55.3%; Score 745.5; DB 12; Length 266;
Best Local Similarity 53.0%; Pred. No. 3.3e-70;
Matches 140; Conservative 50; Mismatches 73; Indels 1; Gaps 1;

QY 1 MKPTTISLLQKYKQDKKRFATITAYDSFAKLPADEGLNVLVGDLSGMTVQGHDSLPV 60
Db 1 MENITVTSLLAMKHGKEKITMLTCYDATFAHTACQAGVEVLVGDLSGMTVQGHDSLPV 60
QY 61 TVADIAYHTAAVRGAPNCLLIADLPFMAVATPEQAFENAAATVVRAGANVVKIEGSEWLV 120
Db 61 TTAETATHVACVRKNGCALILADLPFMANATLEQTFINSTLMQAGAHVVKIEGANWLG 120
QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAQAQLLV 180
Db 121 ESIRLLAERGVPCAHMGLTPQSVNVLGGYKVGQGRLEAQAQRMRADAIALEQAQAAMILL 180
QY 181 ECVPELAKRITERALATPVIGAGNVTGQILVWHDFAFGIT-GGHIKPKAKNPLAETGD 239
Db 181 ECVPELAAEITHAVKIPVIGAGSATDGGVLVLDMLGLSLTGRVPKFKVFMQGPDP 240
QY 240 IRAAVRQYMAEVESGVYFGEHSF 263
Db 241 IQSAIQAVSAVKDVSFFAIEHGF 264

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Search completed: July 29, 2004, 10:40:06
Job time : 47 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: July 29, 2004, 10:27:26 ; Search time 13 Seconds  
(without alignments)  
1057.425 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 1349

Sequence: 1 MKPTTISLLQKVKQDKKREA.....ROYMAEVESGVYPGEHSFH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1345	99.7	264	1 PANB_ECOLI	P31057 escherichia
2	1323	98.1	264	1 PANB_ECOLI	Q8f130 escherichia
3	1296	96.1	264	1 PANB_ECO57	Q8x329 escherichia
4	1243.5	92.2	263	1 PANB_SALTY	Q8zrx0 salmonella
5	1243.5	92.2	264	1 PANB_SALTY	Q8z9d2 salmonella
6	1063.5	78.8	265	1 PANB_YERPE	Q8zBK8 yersinia pe
7	973	72.1	264	1 PANB_VIBVU	Q8dc11 vibrio vuln
8	961	71.2	264	1 PANB_VIBPA	Q87lv2 vibrio para
9	950	70.4	264	1 PANB_VIBCH	Q9kud0 vibrio chol
10	923.5	68.5	267	1 PANB_SCHPO	Q09672 schizosacch
11	922	68.3	264	1 PANB_SHEON	Q8e199 shewanella
12	830	61.5	263	1 PANB_BUCAP	P57293 buchnera ap
13	820	60.8	263	1 PANB_BUCAP	Q8x3u6 buchnera ap
14	795.5	59.0	266	1 PANB_PSEPK	Q88dw9 pseudomonas
15	764.5	56.7	266	1 PANB_PSEFL	Q9zep8 pseudomonas
16	755	56.0	274	1 PANB_RALSO	Q8xw45 ralstonia s
17	745.5	55.3	266	1 PANB_PSESM	Q88q95 pseudomonas
18	739.5	54.1	285	1 PANB_WIGER	Q8d2a5 wigleswort
19	727	53.9	271	1 PANB_XANAC	Q8p111 xanthomonas
20	726	53.8	263	1 PANB_NTIMA	Q9juy0 neisseria m
21	714	52.9	271	1 PANB_XANCP	Q8p3c0 xanthomonas
22	710.5	52.7	272	1 PANB_XYLFA	Q9p9r9 xyella fas
23	710.5	52.7	272	1 PANB_XYLFA	Q87aw0 xyella fas
24	708	52.5	263	1 PANB_NTIMB	Q9j2w6 neisseria m
25	685.5	50.8	266	1 PANB_PSEAE	Q9hw70 pseudomonas
26	627	46.5	279	1 PANB_BACSU	Q9kC87 bacillus ha
27	622	46.1	277	1 PANB_BACSU	P52996 bacillus su
28	613.5	45.5	265	1 PANB_LEPIN	Q8ez98 leptospira
29	612	45.4	270	1 PANB_THETA	Q9x251 thermotoga
30	588.5	43.6	281	1 PANB_MYCTB	Q10505 mycobacteri
31	579.5	43.0	276	1 PANB_CLOAB	Q97f39 clostridium
32	570	42.3	262	1 PANB_PYRAE	Q8zt69 pyrobaculum
33	565.5	41.9	274	1 PANB_CAMJE	Q9p1k1 campylobact

#### ALIGNMENTS

##### RESULT 1

ID	PANB_ECOLI	STANDARD;	PRT;	264 AA.
AC	P31057;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)			
DE	(ketopantoate hydroxymethyltransferase).			
GN	PANB OR B0134.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / W3110;			
RC	Merkel W.K., Nichols B.P.;			
RA	"Nucleotide sequence of the Escherichia coli panBCD gene cluster.";			
RL	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.			
[2]				
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.			
RP	STRAIN=K12;			
RC	MEDLINE=83209595; PubMed=8096212;			
RA	Jones C.E., Brook J.M., Buck D., Abell C., Smith A.G.;			
RT	"Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopantoate hydroxymethyltransferase, and overexpression of the enzyme.";			
RL	J. Bacteriol. 175:2125-2130 (1993).			
[3]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / W3110;			
RC	MEDLINE=94261430; PubMed=8202364;			
RA	Fujita N., Mori H., Yura T., Ishihama A.;			
RT	"Systematic sequencing of the Escherichia coli genome: analysis of the 2.4-4.1 min (110,917-193,643 bp) region.";			
RL	Nucleic Acids Res. 22:1637-1639 (1994).			
[4]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / MG1655;			
RC	MEDLINE=97436617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474 (1997).			
[5]				
RN	SEQUENCE OF 1-12.			
RP	STRAIN=K12 / EMG2;			
RC	MEDLINE=97443975; PubMed=9298646;			
RA	Link A.J., Robison K., Church G.M.;			
RT	"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";			
RL	Electrophoresis 18:1259-1313 (1997).			
CC	-1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-			

Q917b2 mycobacteri  
Q9ams0 bradyrhizob  
Q9cbt0 mycobacteri  
Q92aa6 listeria in  
Q974y0 sulfolobus  
Q9rks2 streptomyce  
Q8y601 listeria mo  
Q67783 aquifex aeo  
Q9x712 corynebacte  
Q931e6 staphylococ  
Q8cr20 staphylococ  
Q8tua5 corynebacte

34 565.5 41.9 280 1 PANB\_MYCVN  
35 559 41.4 298 1 PANB\_BRAJA  
36 556.5 41.3 286 1 PANB\_MYCLE  
37 556 41.2 277 1 PANB\_LISIN  
38 554 41.1 267 1 PANB\_SULTO  
39 549.5 40.7 291 1 PANB\_STROO  
40 546 40.5 277 1 PANB\_LISMO  
41 534 39.6 265 1 PANB\_AQUAE  
42 527.5 39.1 269 1 PANB\_CORGL  
43 526.5 39.0 272 1 PANB\_STAAM  
44 522.5 38.7 272 1 PANB\_STAEP  
45 520.5 38.6 269 1 PANB\_COREF

CC oxobutanate = tetrahydrofolate + 2-dehydropanotoate.  
 CC -|- SUBUNIT: Pantothenate biosynthesis; first branch; first step.  
 CC -|- SIMILARITY: Hexamer (Potential).  
 CC -|- SIMILARITY: Belongs to the panB family.  
 CC -----  
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 CC -----  
 CC EMBL; LI7086; AAA24271.1; -;  
 CC EMBL; X65538; CAA46505.1; -;  
 CC EMBL; D26562; BAB96711.1; -;  
 CC EMBL; AB000122; AAC73245.1; -;  
 CC PIR; F64736; F64736  
 CC ECoGene; EGI1675; panB.  
 CC HAMAP; MF\_00156; -; 1.  
 CC InterPro; IPR003700; Pantoate transf.  
 CC Pfam; PF02548; Pantoate transf; 1.  
 CC TIGRFAMs; TIGR00222; panB; 1.  
 CC Pantothenate biosynthesis; Transferase; Methyltransferase;  
 CC Complete proteome.  
 CC FT CONFLICT 7 8 SL -> AS (IN REF. 2).  
 CC FT CONFLICT 12 12 Y -> C (IN REF. 2).  
 CC FT CONFLICT 15 15 E -> D (IN REF. 2).  
 CC FT CONFLICT 63 63 A -> E (IN REF. 2).  
 CC FT CONFLICT 124 124 Q -> K (IN REF. 2).  
 CC SQ SEQUENCE 264 AA; 28237 MW; 0437D6BB9EBF817B CRC64;

Query Match 99.7%; Score 1345; DB 1; Length 264;  
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;  
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60  
 DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60  
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120  
 DB 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120  
 QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGGRDEAGDQLLSDALALEAQAQLLV 180  
 DB 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGGRDEAGDQLLSDALALEAQAQLLV 180  
 QY 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVROYMAEVESGVYFGEHSFH 264  
 DB 241 RAAVROYMAEVESGVYFGEHSFH 264

RESULT 2  
 PANB\_ECOL6  
 ID PANB\_ECOL6 STANDARD; PRT; 264 AA.  
 AC Q8FL30;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)  
 DE (Ketopantoate hydroxymethyltransferase).  
 GN PANB OR C0165.  
 OS Escherichia coli O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=O6:H1 / CFT073 / ATCC 700928;  
 RX MEDLINE=22388234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 of uropathogenic *Escherichia coli*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).  
 CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanotoate.  
 CC -|- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
 CC -|- SUBUNIT: Hexamer (Potential).  
 CC -|- SIMILARITY: Belongs to the panB family.  
 CC -----  
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 CC -----  
 CC EMBL; AB016755; AAN78659.1; -;  
 CC HAMAP; MF\_00156; -; 1.  
 CC InterPro; IPR003700; Pantoate transf.  
 CC Pfam; PF02548; Pantoate transf; 1.  
 CC TIGRFAMs; TIGR00222; panB; 1.  
 CC Pantothenate biosynthesis; Transferase; Methyltransferase;  
 CC Complete proteome.  
 CC SQ SEQUENCE 264 AA; 28163 MW; CF11D9B42F7B3765 CRC64;

Query Match 98.1%; Score 1323; DB 1; Length 264;  
 Best Local Similarity 98.1%; Pred. No. 1e-98;  
 Matches 259; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60  
 DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60  
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120  
 DB 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120  
 QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGGRDEAGDQLLSDALALEAQAQLLV 180  
 DB 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGGRDEAGDQLLSDALALEAQAQLLV 180  
 QY 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVROYMAEVESGVYFGEHSFH 264  
 DB 241 RAAVROYMAEVESGVYFGEHSFH 264

RESULT 3  
 PANB\_ECO57  
 ID PANB\_ECO57 STANDARD; PRT; 264 AA.  
 AC Q8X329;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)  
 DE (Ketopantoate hydroxymethyltransferase).  
 GN PANB OR Z0145 OR ECS0138.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.





```

3Q SEQUENCE 265 AA; 28699 MW; DC75A16F98A08097 CRC64;

Query Match 78.8%; Score 1063.5; DB 1; Length 265;
Best Local Similarity 76.1%; Pred. No. 5.6e-78;
Matches 201; Conservative 36; Mismatches 26; Indels 1; Gaps 1

  1 MKPTTISLLQYKQDKKRFAITITAYDSYFAKLPADEGLNVLVGDSLGMTVQGHDSITLVP 60
  1 MKTTTMSQLRQWKQEKRRKFAITLTAIDASFAQLPAEQGIQVLLVGDSLGMTLQGFDSITLVP 60
  61 TVADTAYHTAATVRGAPNCLLLADLPMAVATPEQAFENNAATVMRAGANWKIEGEWLV 120
  61 TVADWAYHTRAVRGAPHCLLLADMPMSVATPELATPHTAAELMRAGANWKIEGGSMLC 120
  121 ETVQMLTERAVPVVCGHLGLTPOSVNIFFGGYKVQGRGDEAGDQLLSDALALEAAGQLLV 180
  121 DTRIMLAERAVPVVCGHLGLTPOSVNIFFGYKVQGREEVAANQLQDAIALEAQAQLLV 180
  181 ECVPVYELAKRITEALTPVIGIGAGNVTDCQILVMHDAGFICGTGHTPKAKNFLAET-CD 239
  181 ECVPVYELAQRVTEELTPVIGIGAGNVTDCQILVMHDALGITGHTPKFKNFLAHSAGD 240
  240 TRAAVRQYMAEVESGWYPGEESHF 263
  241 TRAAIKLYIEEVGGIYPAEHTF 264

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RESULT 7
-----
D PANB_VIBUO STANDARD; PRT; 264 AA.
C Q8DC11;
T 10-OCT-2003 (Rel. 42, Created)
T 10-OCT-2003 (Rel. 42, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
E 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
E (Ketopantoate hydroxymethyltransferase).
N PANB OR VU1643.
S Vibrio vulnificus.
S Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
S Vibrionaceae; Vibrio.
X NCBI_TaxID=672;
X [1]
UN SEQUENCE FROM N.A.
RP STRAIN=CMCP6;
CA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
CA Choy H.E.;
CA "Complete genome sequence of Vibrio vulnificus CMCP6."
CA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CA -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
CA oxobutanoate = tetrahydrofolate + 2-dehydropanoate.
CA -!- PATHWAY: Pantothenate biosynthesis; first branch; first step.
CA -!- SIMILARITY: Belongs to the panB family.
CA -----
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CA or send an email to license@isb-sib.ch).
CA -----
CA EMBL; AE016802; AAC10060.1; -.
CA HAMAP; MF_00156; -.
CA InterPro; IPR003700; Pantoate_transf.
CA Pfam; PF02548; Pantoate_transf; 1.
CA TIGRfams; TIGR00222; panB; 1.
CA Pantothenate biosynthesis; Transferase; Methyltransferase;
CA Complete proteome.
CA SEQUENCE 264 AA; 28662 MW; 6C5DC45E1A08474F CRC64;
SQ

```

[illegible][illegible]

Db 1 MKQWINDLWKQKGRKATSTAYDASFAQLFESQEMPVLLVGDLSGLWVLEGNDTLPV 60  
QY 61 TVADIAYHTAAVRGAPNCLLADLPFWAYATPEQAFENAATVVRAGANNVKIKGGWLV 120  
Db 61 TVDDIVYHTRCVRAGSPNCLLMADMPFMSYATPEQACENAAKLVRAGANNVKIKGGWLV 120  
QY 121 ETVOMLTERAVPVCGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALALEAQAQLLV 180  
Db 121 DTVMLETERAVPVCAHLGTPVSNVIFGKVKQGRGDEAGDQLLSDALALEAQAQLLV 180  
QY 181 ECVPELAKRITELALIPVIGAGNVTGQILVMDHAFGITHGHIKPKAFNLAETGDI 240  
Db 181 ECVPAELARITKVLDPVIGAGNVTGQILVMDHAFGITHGHIKPKAFNLAETGDI 240  
QY 241 RAAVROYMAEVESGVYPGEHS 262  
Db 241 RKAVALYIEDVANGVFPDDAHT 262

RESULT 9  
PANB\_VIBCH STANDARD; PRT; 264 AA.  
AC Q9KUD0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)  
DE (Ketopantoate hydroxymethyltransferase).  
GN PANB\_OR VC0592.  
OS Vibrio cholerae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=666;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EI FOR N16961 / Serotype O1;  
RX MEDLINE=20406833; PubMed=10952301;  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,  
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
RA Emwolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
RA McDonald L., Uterback T., Fleischmann R.D., Niernan W.C., White O.,  
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
RA Fraser C.M.;  
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";  
RL Nature 406:477-483 (2000).  
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanotate.  
CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
CC -1- SIMILARITY: Belongs to the panB family.  
CC -----  
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CC -----  
CC EMBL; AE004144; AAF93759.1; --  
CC DR PIR; A82304; A82304.  
CC TIGR; VC0592;  
CC HAMAP; MF\_00156; --; 1.  
CC InterPro; IPR003700; Pantoate transf.  
CC Pfam; PF02548; Pantoate transf; 1.  
CC TIGRFAMs; TIGR00222; panB; 1.  
CC KW Pantothenate biosynthesis; Transferase; Methyltransferase;  
KW Complete proteome.  
SQ SEQUENCE 264 AA; 28659 MW; 68A61A0D979351B3 CRC64;

Query Match 70.4%; Score 950; DB 1; Length 264;  
Best Local Similarity 68.7%; Pred. No. 6.6e-69;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;  
QY 1 MKPTTISLLQKYKQKRRFATITAYDYSFAKLFADEGLNMLYDGLSGLWVLEGNDTLPV 60  
Db 1 MKKTTINDLMKWQKGRKATSTAYDASFAQLFESQEMPVLLVGDLSGLWVLEGNDTLPV 60  
QY 61 TVADIAYHTAAVRGAPNCLLADLPFWAYATPEQAFENAATVVRAGANNVKIKGGWLV 120  
Db 61 TVDDIVYHTRCVRAGSPNCLLMADMPFMSYATPEQACENAAKLVRAGANNVKIKGGWLV 120  
QY 121 ETVOMLTERAVPVCGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALALEAQAQLLV 180  
Db 121 DTVMLETERAVPVCAHLGTPVSNVIFGKVKQGRGDEAGDQLLSDALALEAQAQLLV 180  
QY 181 ECVPELAKRITELALIPVIGAGNVTGQILVMDHAFGITHGHIKPKAFNLAETGDI 240  
Db 181 ECVPAELARITKVLDPVIGAGNVTGQILVMDHAFGITHGHIKPKAFNLAETGDI 240  
QY 241 RAAVROYMAEVESGVYPGEHS 262  
Db 241 RKAVALYIEDVANGVFPDDAHT 262  
RESULT 10  
PANB\_SCHPO STANDARD; PRT; 267 AA.  
AC Q09672;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable 3-methyl-2-oxobutanate hydroxymethyltransferase  
DE (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase).  
GN SPAGSH10.09C.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4996;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21849401; PubMed=11859360;  
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,  
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Borzym K., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Harrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880 (2002).  
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanotate.  
CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
CC -1- SIMILARITY: Belongs to the panB family.  
CC -----

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CC EMBL; Z49811; CA889959.1; --  
 CC PIR; S55487; S55487.  
 CC GeneDB SPombe; SPAC5H10.09c; --  
 CC InterPro; IPR003700; Pantoate transf.  
 CC Pfam; PF02548; Pantoate transf; 1.  
 CC TIGRFAMs; TIGR00222; panB; 1.  
 CC Pantothenate biosynthesis; Transferase; Methyltransferase.  
 CC SEQUENCE 267 AA; 29111 MW; 80B4FE50759960E9 CRC64;

Query Match 68.58; Score 923.5; DB 1; Length 267;  
 Best Local Similarity 68.24; Pred. No. 8.7e-67;  
 Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;

1 MKPTTISLLQKYKQDKRRFATITAYDYSFAKLPADEGLNVLVGLSGMTVQGHSTLTPV 60  
 3 LKQITISTLQWKLANKKFCACITAYDASFSRLPAEQGMPVLMVGLSLGTAQGHSTLTPV 62  
 61 TVADIAVHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAVTMRAGANMKIE-GGSWL 119  
 63 SVEDIAVHTKSVRGAPNRLMLADLPFMSYSTWEDACKNAATVRAGANIVIEGGNWI 122  
 120 VETVQMLTERAVPVCVGHGLTPOSVNIFFGYKVGQGRDEAGDQLLSDALAEAGQALLV 179  
 123 FEIVQRTESVPVAGHLGTLTPOSVNIFFGYKVGQGRDEAGDQLLSDALAEAGQALLV 182  
 180 LECVPVELAKRITTEALAIPIVIGAGNVTGQILVNHDAFGITGGHIPKFAKNFLAETGD 239  
 183 LECIPESLAQIKTKTISPTIGIGAGKHTDQILVNHDAFGITGGHIPKFAKNFLSGAGD 242  
 240 IRAAVROYMAEVESGVYPGEHSF 263  
 243 IRTAIQRIYIEVSGGLYPASEHSF 266

## RESULT 11

PANB SHEON STANDARD; PRT; 264 AA.  
 D PANB SHEON  
 C QBEIG;  
 T 10-OCT-2003 (Rel. 42, Created)  
 T 10-OCT-2003 (Rel. 42, Last sequence update)  
 T 10-OCT-2003 (Rel. 42, Last annotation update)  
 E 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)  
 E (Ketopantoate hydroxymethyltransferase).  
 N PANB OR S00870.  
 N Shewanella oneidensis.  
 C Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 C Alteromonadaceae; Shewanella.  
 X NCBI\_TaxID=70863;  
 N [1]

P SEQUENCE FROM N.A.  
 C STRAIN=MR-1;  
 X MEDLINE=2297686; PubMed=12368813;  
 X Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 A Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,  
 A Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,  
 A DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
 A Madupu R., Peterson J.D., Unayam L.A., White O., Wolf A.M.,  
 A Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,  
 A Mueller J., Khouri H., Gill J., Uitterback T.R., McDonald L.A.,  
 A Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.;  
 T "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 L Nat. Biotechnol. 20:1118-1123 (2002).  
 C -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.

CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
 CC -1- SIMILARITY: Belongs to the panB family.

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CC EMBL; AE015532; AAN53946.1; --  
 CC TIGR; S00870; --  
 CC HAMAP; MF 00156; --; 1.  
 CC InterPro; IPR003700; Pantoate transf.  
 CC Pfam; PF02548; Pantoate transf; 1.  
 CC TIGRFAMs; TIGR00222; panB; 1.  
 CC Pantothenate biosynthesis; Transferase; Methyltransferase;  
 CC Complete proteome.  
 CC SEQUENCE 264 AA; 28208 MW; 87076E62683B9660 CRC64;

Query Match 68.3%; Score 922; DB 1; Length 264;  
 Best Local Similarity 65.2%; Pred. No. 1.1e-66;  
 Matches 172; Conservative 38; Mismatches 54; Indels 0; Gaps 0;

Qy 1 MKPTTISLLQKYKQDKRRFATITAYDYSFAKLPADEGLNVLVGLSGMTVQGHSTLTPV 60  
 Db 1 MSKVTSTLLKYQKGRKFTALTAYDASPAFDGEGIDVLLVGLSLGVLQGHDDTLTPV 60  
 Qy 61 TVADIAVHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAVTMRAGANMKIEGEXLV 120  
 Db 61 TTADIAVHTRCVRRGTERSLLIADPFMSYATPEQAMENATTLMOAGANMKIEGHWLL 120  
 Qy 121 ETVQMLTERAVPVCVGHGLTPOSVNIFFGYKVGQGRDEAGDQLLSDALAEAGQALLV 180  
 Db 121 ETVTKLTERGIPVCAHLGLTPOSVNVVFGKVGQGRDAENAOQRIIDEAKALEAAGQALLV 180  
 Qy 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVNHDAFGITGGHIPKFAKNFLAETGDI 240  
 Db 181 ECIPASLATAITQALTIPVIGAGATTGQILVNHDAFGITGGHIPKFAKNFLAETGDI 240  
 Qy 241 RAAVROYMAEVESGVYPGEHSF 264  
 Db 241 RSAVRAYIEVANGSPFSAETFN 264

## RESULT 12

PANB BUCAI STANDARD; PRT; 263 AA.  
 ID PANB BUCAI  
 AC P57293;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)  
 DE (Ketopantoate hydroxymethyltransferase).  
 GN PANB OR BU197.  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 OS symbiotic bacterium).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 CX NCBI\_TaxID=118099;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Tokyo 1998;  
 RC MEDLINE=20445173; PubMed=10993077;  
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT "Genome sequence of the endocellular bacterial symbiont of aphids  
 RT Buchnera sp. APS.";  
 RL Nature 407:81-86 (2000).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.  
 CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
 CC -1- SIMILARITY: Belongs to the panB family.

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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AP001118; BAB12914.1; -  
 DR HAMAP; MF\_00156; ; 1.  
 DR InterPro; IPR003700; Pantoate transf.  
 DR Pfam; PF02548; Pantoate transf; 1.  
 DR TIGRFAMs; TIGR00222; panB; 1.  
 KW Pantothenate biosynthesis; Transferase; Methyltransferase;  
 KW Complete proteome.  
 SQ SEQUENCE 263 AA; 29353 MW; 2FDA6D9D963B9098 CRC64;  
 Query Match 61.5%; Score 830; DB 1; Length 263;  
 Best Local Similarity 56.7%; Pred. No. 2.5e-59;  
 Matches 149; Conservative 59; Mismatches 55; Indels 0; Gaps 0;  
 QY 1 MKPTTISLQKYKODKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSITLPV 60  
 DB 1 MESITISLQKWKINKKFAAITAYDFSRFLFNCGIPVILIGSLGMIQGHSTLPV 60  
 QY 61 TVADIAHTAAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGHWLV 120  
 DB 61 KTDIAVHTKAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGHWLV 120  
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNI FGKYGKVGQGRDEAGDQLLSDALAEAGQILLV 180  
 DB 121 EIIRLSNLRIICGHIGLIPQSFYLGKYGKVGQGRDEAGDQLLSDALAEAGQILLV 180  
 QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECIPKLAARKITESLIPVIGIGSGKNTDQILVMHDLGITEGKTPSFYKFNFLSESDSI 240  
 QY 241 RAAVROYMAEVESGYPGGEHSF 263  
 DB 241 QKAIQYIYEVEHSYPSKGSF 263  
 RESULT 13  
 PANE\_BUCAP  
 ID PANE\_BUCAP STANDARD; PRT; 263 AA.  
 AC Q8K906;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)  
 DE (Ketopantoate hydroxymethyltransferase).  
 GN PANE OR BUSG191.  
 OS Buchnera aphidicola (subsp. Schizaphis graminum).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=98794;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22084549; PubMed=12089438;  
 RA Tamas I., Klasson L., Cambaek B., Naeslund A.K., Eriksson A.-S.,  
 RA Werngreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;  
 RT "50 million years of genomic stasis in endosymbiotic bacteria";  
 RL Science 296:2376-2379(2002).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.  
 CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
 CC -1- SIMILARITY: Belongs to the panB family.  
 CC -----  
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 -----  
 EMBL; AE014095; AAM67756.1; -  
 DR HAMAP; MF\_00156; ; 1.  
 DR InterPro; IPR003700; Pantoate transf.  
 DR Pfam; PF02548; Pantoate transf; 1.  
 DR TIGRFAMs; TIGR00222; panB; 1.  
 KW Pantothenate biosynthesis; Transferase; Methyltransferase;  
 KW Complete proteome.  
 SQ SEQUENCE 263 AA; 29352 MW; 8AF9B8E12BC5ACA4 CRC64;  
 Query Match 60.8%; Score 820; DB 1; Length 263;  
 Best Local Similarity 57.4%; Pred. No. 1.6e-58;  
 Matches 151; Conservative 55; Mismatches 57; Indels 0; Gaps 0;  
 QY 1 MKPTTISLQKYKODKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSITLPV 60  
 DB 1 MESITISLQKWKINKKFAAITAYDFSRFLFNCGIPVILIGSLGMIQGHSTLPV 60  
 QY 61 TVADIAHTAAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGHWLV 120  
 DB 61 KTDIAVHTKAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGHWLV 120  
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNI FGKYGKVGQGRDEAGDQLLSDALAEAGQILLV 180  
 DB 121 ETVKELSKRSLVCHGLTPOSVNI FGKYGKVGQGRDEAGDQLLSDALAEAGQILLV 180  
 QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECIPSLAKKITEALAIPIVIGAGNVTGQILVMHDLGITEGKTPSFYKFNFLCHNGSI 240  
 QY 241 RAAVROYMAEVESGYPGGEHSF 263  
 DB 241 QKAIQYIYEVEHSYPSKYSF 263  
 RESULT 14  
 PANE\_PSEPK  
 ID PANE\_PSEPK STANDARD; PRT; 266 AA.  
 AC Q8DW9;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)  
 DE (Ketopantoate hydroxymethyltransferase).  
 GN PANE OR PP4699.  
 OS Pseudomonas putida (strain KT2440).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=160488;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22423060; PubMed=12534463;  
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,  
 RA Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,  
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,  
 RA Urtabek T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,  
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,  
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoef A., Tummeler B.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence and comparative analysis of the  
 RT metabolically versatile Pseudomonas putida KT2440";  
 RL Environ. Microbiol. 4:799-808(2002).  
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.  
 CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
 CC -1- SIMILARITY: Belongs to the panB family.  
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R EMBL; AB016791; AAN70272.1; -;  
R TIGR; PA4699; -;  
R HAMAP; MF\_00156; -; 1.  
R InterPro; IPR003700; Pantoate transf.  
R Pfam; PF02548; Pantoate transf; 1.  
W Pantothenate biosynthesis; Transferase; Methyltransferase;  
W Complete proteome.  
Q SEQUENCE 266 AA; 2762 MW; D2CF23D7E7E15001 CRC64;

Query Match 59.0%; Score 795.5; DB 1; Length 266;  
Best Local Similarity 56.8%; Pred. No. 1.5e-56;  
Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;

Y 1 MKPTTISLLOKQKQKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQGHDSILPV 60  
b 1 MPEVTLTTLNGLKAKGKITMLTCYDATFAKASQAGVEVLVGDLSLGMTVQGHDSILPV 60  
Y 61 TVADIAVHTAAVRGAPNCLLADLPFAYATPEQAFENAAATVWRAGANMVKIEGWL 120  
b 61 TTAEMAYHTASVKGNDGALITLDPFMAHATPEQAFANSAATLMQAGAHMVKIEGA 120  
Y 121 ETQVQLTERAVPVCGLHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQL 180  
b 121 ETIRLLAERGVPVCAHMGGLTPQVNVLLGGYKVGQROEQARQMRADALEAQA 180  
Y 181 ECVPELAKRITTEALAIPTVIGAGNVTGQILVMDAFGIT-GGHIPKFAKNFLAETGD 239  
b 181 ECVPELAAEITNAVGLPVGIGAGSATDQVLLVHDMGLSLGRVPKFKVNFMTG 240  
Y 240 IRAAVROYMAEVSGVYPGEHSF 263  
b 241 IHSALVAYVEAVKVSFPGSEHGF 264

RESULT 15

ANB\_PSEFL PANB\_PSEFL STANDARD; PRT; 266 AA.  
C Q9ZER8:  
Y 16-OCT-2001 (Rel. 40, Created)  
Y 16-OCT-2001 (Rel. 40, Last sequence update)  
Y 28-FEB-2003 (Rel. 41, Last annotation update)  
Y 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.1.2.11)  
Y (Ketopantoate hydroxymethyltransferase).  
Y PANB.  
Y Pseudomonas fluorescens.  
Y Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Y Pseudomonadaceae; Pseudomonas.  
Y NCBI\_TaxID=294;  
Y [1]  
Y SEQUENCE FROM N.A.  
Y STRAIN=SBW25;  
Y Rainey P. B.;

Y "Adaptation of Pseudomonas fluorescens to the plant rhizosphere."  
Y Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
Y -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.  
Y -!- PATHWAY: Pantothenate biosynthesis; first branch; first step.  
Y -!- SIMILARITY: Belongs to the panB family.

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CC EMBL; AUI30846; CAA10222.1; -;  
DR HAMAP; MF\_00156; -; 1.  
DR InterPro; IPR003700; Pantoate transf.  
DR Pfam; PF02548; Pantoate transf; 1.  
DR TIGRPFAMs; TIGR00222; panB; 1.  
KW Pantothenate biosynthesis; Transferase; Methyltransferase.  
SQ SEQUENCE 266 AA; 2762 MW; 51B59D25C30B03F3 CRC64;

Query Match 56.7%; Score 764.5; DB 1; Length 266;  
Best Local Similarity 53.4%; Pred. No. 4.4e-54;  
Matches 141; Conservative 49; Mismatches 73; Indels 1; Gaps 1;

Qy 1 MKPTTISLLOKQKQKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQGHDSILPV 60  
Db 1 MPDITLITLQSLKLGKIKITMLTCYDATFAHASQAGIEVLVGDLSLGMTVQGHDSILPV 60  
Qy 61 TVADIAVHTAAVRGAPNCLLADLPFAYATPEQAFENAAATVWRAGANMVKIEGWL 120  
Db 61 TTDELAHTASVKGNDGAFITADLPFMYATPEQAFENAAATVWRAGANMVKIEGWL 120  
Qy 121 ETQVQLTERAVPVCGLHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQL 180  
Db 121 ESIRLLAERGVPVCAHMGGLTPQSVNLLGGYKVGQNEAQAQMRADALEAQA 180  
Qy 181 ECVPELAKRITTEALAIPTVIGAGNVTGQILVMDAFGIT-GGHIPKFAKNFLAETGD 239  
Db 181 ECVPELAAEITQAVKVPVIGIGAGSATDQVLLVHDMGLSLGRVPKFKVNFMTG 240  
Qy 240 IRAAVROYMAEVSGVYPGEHSF 263  
Db 241 IHDALSAYVAEVKGVTFPGAHEGF 264

Search completed: July 29, 2004, 10:33:40  
Job time : 14 secs



GenCore version 5.1.6  
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XM protein - protein search, using sw model

run on: July 29, 2004, 10:30:36 ; Search time 39 Seconds  
(without alignments)  
2135.816 Million cell updates/sec

Title: US-09-820-745-7  
Perfect score: 1349  
Sequence: 1 MKPTTISLLQKYQDKKREA.....RQVMAEVESGVYPGBEHSFH 264

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 315518202 residues  
total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archae:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	97.9	254	16 Q83MES	Q83mes shigella fl
2	795.5	59.0	266	16 Q88DW9	Q88dw9 pseudomonas
3	789.5	58.5	266	2 Q848I7	Q848i7 pseudomonas
4	745.5	55.3	266	16 Q888Q5	Q888q5 pseudomonas
5	631.5	46.8	269	16 Q82Y18	Q82y18 nitrosomona
6	616	45.7	277	2 Q8GDR8	Q8gdr8 heliobacill
7	604	44.8	278	16 Q81FN7	Q81fn7 bacillus ce
8	601	44.6	279	16 Q81ST3	Q81st3 bacillus an
9	598.5	44.4	275	16 Q833S5	Q833s5 enterococcu
10	547.5	40.6	287	16 Q82AW2	Q82aw2 streptomyce
11	516.5	38.3	266	16 Q83EA2	Q83ea2 coxiella bu
12	509	37.7	269	16 Q7UM39	Q7um39 rhodopirell
13	489.5	36.3	271	2 Q841Y3	Q841y3 campylobact
14	485.5	36.0	273	16 Q8A9W7	Q8a9w7 bacteroides
15	476.5	35.3	347	10 Q82357	Q82357 arabidopsis
16	470	34.8	278	16 Q7WER7	Q7wer7 bordetella

17	470	34.8	278	16 Q7W3E7	Q7w3e7 bordetella
18	470	34.5	354	16 Q7VW53	Q7vw53 bordetella
19	465.5	34.5	354	10 Q9M315	Q9m315 arabidopsis
20	459	34.0	364	10 Q9AWZ8	Q9awz8 oryza sativ
21	456	33.8	273	16 Q89MZ4	Q89mz4 bradyrhizob
22	452.5	33.5	399	10 Q9AWZ7	Q9awz7 oryza sativ
23	449.5	33.3	269	16 Q83HM1	Q83hm1 tropheryma
24	449.5	33.3	272	16 Q83GX7	Q83gx7 tropheryma
25	448.5	33.2	284	16 Q7VIU7	Q7viu7 halicobacte
26	439.5	32.6	178	2 Q7WU77	Q7wu77 thermotoga
27	439	32.5	252	16 Q9A7R9	Q9a7r9 caulobacter
28	414	30.7	326	16 Q89T26	Q89t26 bradyrhizob
29	411	30.5	269	2 Q8RJE2	Q8rje2 rhizobium l
30	393.5	29.2	257	2 Q9RLE2	Q9rle2 prochloroco
31	393.5	29.2	257	16 Q7TU60	Q7tu60 prochloroco
32	390	28.9	267	16 Q7TUU0	Q7ttu0 synecchococ
33	388	28.8	256	16 Q93JX5	Q93jx5 prochloroco
34	376	27.9	272	16 Q7TV48	Q7tv48 prochloroco
35	287.5	21.3	192	10 Q94GC9	Q94gc9 solanum dem
36	275.5	20.4	267	16 Q98JY0	Q98jy0 rhizobium l
37	254	18.8	90	2 Q7X234	Q7x234 alteromonas
38	251	18.6	266	2 Q989M7	Q989m7 rhizobium m
39	242	17.9	286	16 Q92VY6	Q92vy6 rhizobium m
40	239	17.7	270	16 Q985K7	Q985k7 rhizobium l
41	113.5	8.4	356	5 Q8MRV9	Q8mr9 drosophila
42	109	8.1	1166	2 Q8VSB0	Q8vsb0 shigella fl
43	109	8.1	1623	2 Q9AFLO	Q9aflo shigella fl
44	105	7.8	287	16 Q8YVW0	Q8yvw0 anabaena sp
45	105	7.8	877	16 Q8XSY7	Q8xsy7 ralstonia s

## ALIGNMENTS

## RESULT 1

Q83MES	ID	Q83MES	PRELIMINARY;	PRT;	264 AA.
AC	Q83MES;				
DT	01-JUN-2003 (TrEMBLrel. 24, Created)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).				
GN	PANB OR SF0131 OR S0133.				
OS	Shigella flexneri.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Shigella.				
OX	NCBI_TaxID=623;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=301 / Serotype 2a;				
RX	MEDLINE=22272406; PubMed=12384590;				
RA	Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,				
RA	Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,				
RA	Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,				
RA	Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,				
RA	Yu J.;				
RT	"Genome sequence of Shigella flexneri 2a: insights into pathogenicity				
RT	through comparison with genomes of Escherichia coli K12 and O157.";				
RL	Nucleic Acids Res. 30:4432-4441(2002).				
RP	[2]				
RC	SEQUENCE FROM N.A.				
RX	STRAIN=2457T / ATCC 700930 / Serotype 2a;				
RA	MEDLINE=22550274; PubMed=12704152;				
RA	Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,				
RA	Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,				
RA	Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,				
RA	Schwartz D.C., Blattner F.R.;				
RT	"Complete genome sequence and comparative genomics of Shigella				
RT	flexneri serotype 2a strain 2457T.";				
RL	Infect. Immun. 71:2775-2786(2003).				
DR	EMBL; AE015050; AAN41794.1; -				
DR	EMBL; AE016978; AAP15675.1; -				
DR	GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. .; IEA.				



DB 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKFNFLAETGDI 240  
2Y 240 IRAAVROYMAEVESGVYPGEHSF 263  
DB 241 IQGALSAYVAEKAATPGVEHGF 264

RESULT 4  
Q88805 PRELIMINARY; PRT; 266 AA.  
AC Q88805;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase.  
DN PANB OR NSPT00961.  
DS Pseudomonas syringae (pv. tomato).  
DC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
DC Pseudomonadaceae; Pseudomonas.  
DX NCBI\_TaxID=323;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DC3000;  
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,  
RA Berry K., Utechtack T., Van Aken S., Feldblyum T., Gwinn M.,  
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,  
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidse T.,  
RA White O., Fraser C., Collier A.,  
RA "Complete sequence of Pseudomonas syringae."  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RJ EMBL; AE016859; AA054495.1; -.  
JR TIGR; PSPT00961; -.  
RR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . . ; IEA.  
RR GO; GO:0008168; F:methyltransferase activity; IEA.  
RR GO; GO:0016740; F:transferase activity; IEA.  
RR GO; GO:0015940; P:pantothenate biosynthesis; IEA.  
RR InterPro: IPR003700; Pantoate transf.  
RR Pfam: PF02548; Pantoate transf. 1.  
RW Transferase; Methyltransferase; Complete proteome.  
RQ SEQUENCE 266 AA; 28074 MW; DC8A1C0D2434E482 CRC64;

Query Match 55.3%; Score 745.5; DB 16; Length 266;  
Best Local Similarity 53.0%; Pred. No. 1e-50;  
Matches 140; Conservative 50; Mismatches 73; Indels 1; Gaps 1;

Y 1 MKPTTISLLQYKQDKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMVTQGHDSITLPTV 60  
b 1 MPNITVTSLAMKHKGEKITMTCYDATFAATACQAGVEVLLIGDSLGLVQLQGHDSITLPTV 60

Y 61 TVADIAVHTAAVRGAPNCILLADLPFMAYATPEQAFENAAVTMRAGANNVKIEGEMVLV 120  
b 61 TTAETAHVAVACVRKGNQGAAILADLPFMANATLEQTFINSTLMQAGAHMKVEGAALWG 120

Y 121 ETVQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGALLVL 180  
b 121 ESIRLLAERGI PVCAHMLGTPQSVNIFGGYKVGQGRLEAQAQWRADALEAAGAMILL 180

Y 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKFNFLAETGDI 239  
b 181 ECVPSELAESIHTAVKIPVIGAGNVTGQVLVHDMGLSLTGRVFKPKFNFLAETGDI 240

Y 240 IRAAVROYMAEVESGVYPGEHSF 263  
b 241 IQSNAIQVSAVKDVSPFAIEHGF 264

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Ketopantoate hydroxymethyltransferase (EC 2.1.2.11).  
GN PANB OR NE0072.  
OS Nitrosomonas europaea.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
OX NCBI\_TaxID=915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19718 / IFO 14298;  
RX MEDLINE=22586410; PubMed=12700255;  
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,  
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;  
RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
obligate chemolithoautotroph Nitrosomonas europaea."  
RL J. Bacteriol. 185:2759-2773 (2003).  
DR EMBL; BX321856; CAD83983.1; -.  
DR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . . ; IEA.  
DR GO; GO:0008168; F:methyltransferase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.  
DR InterPro: IPR003700; Pantoate transf.  
DR Pfam: PF02548; Pantoate transf. 1.  
DR TIGRFAMs; TIGR00222; panB; 1.  
KW Methyltransferase; Transferase; Complete proteome.  
SQ SEQUENCE 269 AA; 28903 MW; 05F99C2CF3E5B13B CRC64;

Query Match 46.8%; Score 631.5; DB 16; Length 269;  
Best Local Similarity 45.8%; Pred. No. 1e-41;  
Matches 120; Conservative 52; Mismatches 90; Indels 1; Gaps 1;

QY 2 KPTTISLLQYKQDKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMVTQGHDSITLPTV 61  
Db 7 KRWITITLQACQGEKIALVTCYDATFAVLEEAGVDILLVGDLSLGMVTQGHDSITLPTV 66

QY 62 VADIAVHTAAVRGAPNCILLADLPFMAY-ATPEQAFENAAVTMRAGANNVKIEGEMVLV 120  
Db 67 LDEMIYHVRVCRVERGTHRVFIMADMPFGTFQVSPQEAFGNAVLMAAGQMVKIEGQHMA 126

QY 121 ETVQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGALLVL 180  
Db 127 ETVEFLSCRGIPVCAHMLGMPQFVHOLGGYRQGTNDARQLREDALLQFAGAMILL 186

QY 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKFNFLAETGDI 240  
Db 187 ELIPAVLGEIEITLLSIPTIGIGAGAACGQVLVHDMGLSGTLPFRVFNFMMDADSI 246

QY 241 IRAAVROYMAEVESGVYPGEHSF 263  
Db 247 QTAVSNYVRAVKLGAPFAVEHTF 269

RESULT 6  
Q8GDR8 PRELIMINARY; PRT; 277 AA.  
AC Q8GDR8;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Fragment).  
DS Helicobacter mobilis.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;  
OC Helicobacteriaceae.  
OX NCBI\_TaxID=28064;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22337798; PubMed=12446909;  
RA Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,  
RA Blankenship R.E.;  
RT "Whole-genome analysis of photosynthetic prokaryotes."  
RL Science 298:1616-1620 (2002).

RN  
 RP SEQUENCE FROM N.A.  
 RA Liolios K.G., Chu L., Ostrovskaya O., Mendybaeva N., Koukharenko V.,  
 RL Gerdes S., Kyrpides N., Overbeek R.,  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY142907; XAN87511.1; -  
 DR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . . ; IEA.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.  
 DR InterPro; IPR003700; Pantoate\_transf.  
 DR Pfam; PF02548; Pantoate\_transf; 1.  
 DR TIGRFAMs; TIGR00222; panB; 1.  
 KW Transferase; Methyltransferase.  
 FT NON\_TER 277  
 SQ SEQUENCE 277 AA; 30137 MW; 1EA3773BB9B3D1E0 CRC64;  
  
 Query Match 45.7%; Score 616; DB 2; Length 277;  
 Best Local Similarity 47.0%; Pred. NO. 1.7e-40;  
 Matches 124; Conservative 50; Mismatches 88; Indels 2; Gaps 2;  
  
 QY 2 KPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNMLVGLSLGTMVQGHSTLPTV 61  
 DB 3 KKITLPQFKRQEQKKRFMTAYDYPPAQLVDSEVEVILVGLSLGMVLGYDSTVPVT 62  
  
 QY 62 VADIAYHTAAVRGAPNCLLLADLPFMAV-ATPEQAFENAAATVNR-AGANMKVKEGGEWL 119  
 DB 63 LBEIMHHCPRVVKGAPHTLVADMPFGTYNTISKDAIRNANRMLKESGIEAVKLEGGKV 122  
  
 QY 120 VETVQMLTERAVPVCGHLGLTPOSVNI FGGYKVGQGRDEAGDQLLSDALALEAQAQLL 179  
 DB 123 APIEAVDAGIPVAGHGLTTPQTAQGLGGFKVQKTEAAQQLLEALALEKAGASLV 182  
  
 QY 180 LECVPVELAKRITAEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGD 239  
 DB 183 IECVPADVARRITEALSIFITIGAGPYCDGQVLVQDMLGMFDRFPTPKFVKYANIGPT 242  
  
 QY 240 IRAAVRQYMAEVESGVYPGEHSF 263  
 DB 243 IREALNTYAQEVSDGTFPGPEYSF 266  
  
 RESULT 7  
 Q81FN7 PRELIMINARY; PRT; 278 AA.  
 AC Q81FN7  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE 3-methyl-2-oxobutanate hydroxymethyltransferase (SC 2.1.2.11).  
 GN BC1540.  
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haseikorn R., Fonstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.;  
 RP "Genome sequence of Bacillus cereus and comparative analysis with  
 RT Bacillus anthracis";  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE017002; AAP08520.1; -  
 DR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . . ; IEA.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.  
 DR InterPro; IPR003700; Pantoate\_transf.  
 DR Pfam; PF02548; Pantoate\_transf; 1.  
 DR TIGRFAMs; TIGR00222; panB; 1.  
 KW Methyltransferase; Transferase; Complete proteome.  
 SQ SEQUENCE 278 AA; 30499 MW; BFE84B585D51E89 CRC64;  
  
 Query Match 44.8%; Score 604; DB 16; Length 278;  
 Best Local Similarity 46.4%; Pred. NO. 1.5e-39;  
 Matches 123; Conservative 50; Mismatches 88; Indels 4; Gaps 3;  
  
 QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNMLVGLSLGTMVQGHSTLPTV 60  
 DB 1 MKTITDDEL--KMKEQGEPIITMLTAYDYPSSAKLAEEAEVDMILVGLSLGMVLGYDSTVPV 58  
  
 QY 61 TVADIAYHTAAVRGAPNCLLLADLPFMAV-ATPEQAFENAAATVNR-AGANMKVKEGGEW 118  
 DB 59 TVEDMIHHTKAVRGAKETFIIVDMPFMSVHVSQETMWNARRIVQESGAHALKVEGAGE 118  
  
 QY 119 LVETVQMLTERAVPVCGHLGLTPOSVNI FGGYKVGQGRDEAGDQLLSDALALEAQAQLL 178  
 DB 119 VISITQVLTNAGIPVWAHLGLTPQSVGLGKVGQKDAESAKKLIEDAKCKCEAGAIAL 178  
  
 QY 179 VLECPVELAKRITAEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETG 238  
 DB 179 VLECPVQMLABELISEQITPTIGIGAGQKVDGQVLVHDLISYGNRVPKFKYQVTSVQE 238  
  
 QY 239 DIRAAVRQYMAEVESGVYPGEHSF 263  
 DB 239 EIVRGISQYVTEVKTQFPPEKHSF 263  
  
 RESULT 8  
 Q81ST3 PRELIMINARY; PRT; 279 AA.  
 AC Q81ST3  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE 3-methyl-2-oxobutanate hydroxymethyltransferase.  
 GN PANB OR BA1562.  
 OS Bacillus anthracis (strain Ames).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=198094;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=12721629;  
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,  
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,  
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,  
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gunn M.,  
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,  
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
 RA Thonason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,  
 RA Fraser C.M.;  
 RP "The genome sequence of Bacillus anthracis Ames and comparison to  
 RT closely related bacteria";  
 RL Nature 423:81-86(2003).  
 DR EMBL; AE017029; AAP25498.1; -  
 DR TIGR; BA1562; -  
 DR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . . ; IEA.  
 DR GO; GO:0008168; F:methyltransferase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.  
 DR InterPro; IPR003700; Pantoate\_transf.  
 DR Pfam; PF02548; Pantoate\_transf; 1.  
 DR TIGRFAMs; TIGR00222; panB; 1.  
 KW Methyltransferase; Transferase; Complete proteome.  
 SQ SEQUENCE 279 AA; 30535 MW; BC891620D7C0D1D6 CRC64;  
  
 Query Match 44.6%; Score 601; DB 16; Length 279;  
 Best Local Similarity 46.4%; Pred. NO. 2.7e-39;  
 Matches 123; Conservative 49; Mismatches 89; Indels 4; Gaps 3;

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2Y 1 MKPTTISLLQKYKQDKKFAITAYDYSFAKLPFADEGLNMLVGDLSGMTVQGHSTLPV 60
Db 1 MKTKDFL--KKKQGEPTIMLTAYDYPKLABEAEVMDILVGDLSGMTVGLYDSTVPV 58
2Y 61 TVADIATHTAARRGAPNCLLLADLPFMAV-ATPEQAFENAAATVMR-AGANMVKIEGGEW 118
Db 59 TVEDMIHTKAARRGAKETFTVTDMPFMSYHVSILQDTMVNARRIVQESGAHALKVBEGAGE 118
2Y 119 LVEITVQMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAQAQLL 178
Db 119 VISTIHVLTNAGIPVVAHLGTLTPQSVGLVGGYKVGQKDAESAKKLIEDAKCKEEAGAIAL 178
2Y 179 VLECVVPVELAKRITEALAIPIVIGAGNVTGQILVNMHDAFGITGGHIFKFAKNVLAETG 238
Db 179 VLECVVPCLAEILISEQLTIPIGIGAGQKVDGQVLVYHDLISIVGVRVRFKVKQYTSVQE 238
2Y 239 DIRAARQYMAEVSGVYPGEHSF 263
Db 239 EIVRISQYVAEVKTRQFPPEKHSF 263

RESULT 9
ID Q833S5 PRELIMINARY; PRT; 275 AA.
AC Q833S5;
CT 01-JUN-2003 (TrEMBLrel. 24, Created)
JT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
JT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
JE 3-methyl-2-oxobutanate hydroxymethyltransferase.
JN PANB OR EF1860.
JS Enterococcus faecalis (Streptococcus faecalis).
JC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
JX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vanathavan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Urrutack T., Redune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RA "Role of mobile DNA in the evolution of vancomycin-resistant
RA Enterococcus faecalis";
RA Science 299:2071-2074 (2003).
RL EMBL; AE016952; AAC81618.1; -.
RR TIGR; EF1860; -.
RR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . .; IEA.
RR GO; GO:0008168; F:methyltransferase activity; IEA.
RR GO; GO:0016740; F:transferase activity; IEA.
RR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
RR InterPro; IPR003700; Pantoate transf.
RR Pfam; PF02548; Pantoate transf. 1.
RR TIGRFAMs; TIGR00222; panB; 1.
RR Methyltransferase; Transferase; Complete proteome.
RR SEQUENCE 275 AA; 29823 MW; 3D3DA408EDAD42FE CRC64;

Query Match 44.4%; Score 598.5; DB 16; Length 275;
Best Local Similarity 45.5%; Pred. No. 4.1e-39;
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

Y 1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPFADEGLNMLVGDLSGMTVQGHST 57
b 1 MKNTAVT---FKESKLREKLMLTAYDYSTAKIIDEAGINILVGDLSGMTVCLGHEDT 56
Y 58 LPVTADIAVHTAAVRGAPNCLLLADLPFMAVATP-EQAFENAAATVMR-AGANMVKIEG 115
b 57 LSVTMDMIHTHTAVTGAKNTLVADMPFMSQTSVDSVNVNAGRLKEGRAQVVKLEG 116
Y 116 GEWLVETVQMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAGA 175
b 117 GIEVCDKIEAIVRASIPVMAHIGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAGA 176
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QY 176 QLLVLECVVPVELAKRITEALAIPIVIGAGNVTGQILVNMHDAFGITGGHIFKFAKNFLA 235
Db 177 FAVVLECVPTKLAELISKETSIPTIGIGAGCGDQILVVDMLGMSYDTPKFKVKKYAN 236
QY 236 ETGDIRAARQYMAEVSGVYPGEHSF 263
Db 237 LSEENKAFTKYIEEVKDGVPFGPEHGF 264

RESULT 10
Q82AW2
ID Q82AW2 PRELIMINARY; PRT; 287 AA.
AC Q82AW2;
CT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative 3-methyl-2-oxobutanate hydroxymethyltransferase.
GN PANB OR SAV5943.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RA avermitilis: deducing the ability of producing secondary
RA metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RA microorganism Streptomyces avermitilis";
RA Nat. Biotechnol. 21:526-531 (2003).
RR EMBL; AP005044; BAC73655.1; -.
RR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . .; IEA.
RR GO; GO:0008168; F:methyltransferase activity; IEA.
RR GO; GO:0016740; F:transferase activity; IEA.
RR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
RR InterPro; IPR003700; Pantoate transf. 1.
RR Pfam; PF02548; Pantoate transf. panB; 1.
RR TIGRFAMs; TIGR00222; panB; 1.
RR Methyltransferase; Transferase; Complete proteome.
RR SEQUENCE 287 AA; 30366 MW; D84BABE213AA76D6 CRC64;

Query Match 40.8%; Score 547.5; DB 16; Length 287;
Best Local Similarity 44.7%; Pred. No. 4.5e-35;
Matches 119; Conservative 46; Mismatches 90; Indels 11; Gaps 5;

Y 5 TISLLQKYKQDKKRFATITAYDYSFAKLPFADEGLNMLVGDLSGMTVQGHSTLPVTVD 64
Db 27 TIRDTTAKERGEKFMILTAYDAMTASVFDEAGIPMLVGDLSAGNCHLYGTYETTVPTLDE 86
QY 65 IAHVHTAAVRGAPNCLLLADLPFMAVATP-EQAFENAAATVMR-AGANMVKIEGGSWLVET 122
Db 87 MTLSAAVVRGTSRALIVGDLFPFGSYQEGPVQALRSATRLVKEAGVAVKLEGGSRSHQ 146
QY 123 VQMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAQAQLLVLEC 182
Db 147 IELVESGIPVMAHIGLTPQSVNAM-GYRVQGRGEAAQQLLRDRAKAVQDAGAFVLEL 205
QY 183 VPVELAKRITEALAIPIVIGAGNVTGQILVNMHDAFGITGGHIFKFAKNFLAETGDIRA 242
Db 206 VPALAEAVTRVLHIPTVGIGAGPETDAQVLVWTDMLGLTGKVPKFKYK---ADLRE 261
```

Thu Jul 29 15:06:38 2004

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QY 243 ----AVRQYMAVESGVYPGEHSF 264
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).
DB 262 VNGNAKAFADVDVGGTFPLEHSVH 287

RESULT 11
Q83EA2 PRELIMINARY; PRT; 266 AA.
AC Q83EA2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase.
GN PANB OR CB0424.
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coccidiaceae; Coccidia.
OX NCBI_TaxID=777;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=2260857; PubMed=12704232;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Daviden T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Knouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RA "Complete genome sequence of the Q-fever pathogen, Coccidia
burnetii."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460 (2003).
RL EMBL; A0016961; AAC89976.1; -.
DR TIGR; CB0424.
DR GO; GO:0003664; F.3-methyl-2-oxobutanoate hydroxymethyltransf. . . ; IEA.
DR GO; GO:0008168; F-methyltransferase activity; IEA.
DR GO; GO:0016740; F-transferase activity; IEA.
DR GO; GO:0015940; P-pantothenate biosynthesis; IEA.
DR InterPro; IPR003700; Pantoate transf.
DR Pfam; PF02548; Pantoate transf. 1.
DR TIGRfam; TIGR00222; panB; 1.
KW Methyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 266 AA; 28996 MW; 744579EC5B46C704 CRC64;

Query Match 38.3%; Score 516.5; DB 16; Length 266;
Best Local Similarity 42.0%; Pred. No. 1.1e-32;
Matches 108; Conservative 48; Mismatches 98; Indels 3; Gaps 3;

QY 10 QYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSITLPTVTVADIAVHT 69
DB 10 QRMKKDKKISVMTCYDYNSACIIQSNDVCLVGDLSLVAMVYGHSTITLPTATVIMAQHI 69
QY 70 AAVRGAPNCLLIADLPFMAATPEQAFENAA-TVWRAGANNVKEGGE-WLWETVQMLT 127
DB 70 QAVSRGAPNKFIIQDNPFCSYKDLTTSNVAERLWQAGQAILEGADAENLKFHHVV 129
QY 128 ERAPVVGHLGTPQSNVTFGGYKVGQGRDEAGDQLSDALEAAGQLVLCVPEL 187
DB 130 KSGIPVIGHLGTPQSIYTLGGFKVQGRKPSAAKIMADAKALAFGTGFAVVLCEVPSL 189
QY 188 AKSITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDIRAAVQY 247
DB 190 AELITHSISITPIGAGPATSGQVLVQLDGLTGNQPKYKLFNGFLIKKALDDF 249
QY 248 MAEVESGVYPG-EEHSF 263
DB 250 DQEVKTSYPLETHCY 266

RESULT 12
Q7UM39 PRELIMINARY; PRT; 269 AA.
ID Q7UM39
AC Q7UM39;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).
GN PANB OR RE0990.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RA "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
RL EMBL; BX294148; CAD76078.1; -.
KW Methyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 269 AA; 28931 MW; 44057A94AABC74A9 CRC64;

Query Match 37.7%; Score 509; DB 16; Length 269;
Best Local Similarity 39.3%; Pred. No. 4.4e-32;
Matches 105; Conservative 54; Mismatches 90; Indels 18; Gaps 4;

QY 5 TISLQYKQKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSITLPTVTVAD 64
DB 12 TTRTLQMRDRGERITWLTAYDPTAKILDEAGVLLVGDITVGMVVGQHSITLPTVMDQ 71
QY 65 IAYHTAAVRGAPNCLLIADLPFMAATPEQAFENAA-TVWRAGANNV-----VKIEG 116
DB 72 MYHAEVMVGRADAMVVDLPF-----PDGDLHLHSV-RCGARVLKETQCHAVKLEG 125
QY 117 EWLVTQMLTERAVPVCGHLGTPQSNVTFGGYKVGQGRDEAGDQLSDALEAAGAQ 176
DB 126 AEQARTEAMVGAGIPVMAHIGLFPQNHVEGGYRLQ----RDIERLVADAKAAEAGAF 181
QY 177 LLVLECVPELAKITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAE 236
DB 182 TVLIECVPESEAAAITDAVKVPTIGAGRDVSGQVLVTHDILGLTSGYTPKTRFLFADV 241
QY 237 TGDTRAAVRQYMAVESGVYPGEHSF 263
DB 242 GNTREAAKSYCDEVKAASFPSDAESF 268

RESULT 13
Q841Y3 PRELIMINARY; PRT; 271 AA.
ID Q841Y3
AC Q841Y3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative 3-methyl-2-oxobutanoate hydroxymethyltransferase.
GN PANB.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=196;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=23D.
RX MEDLINE=90354448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RA "Surface array protein of Campylobacter fetus. Cloning and gene
structure."
RL J. Biol. Chem. 265:14529-14535 (1990).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=23D.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;

```





Thu Jul 29 15:06:38 2004

Search completed: July 29, 2004, 10:34:31  
Job time : 41 secs

GN AT2G46110.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20083487; PubMed=10617197;  
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana";  
RL Nature 402:761-768(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Lin X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,  
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yanada K., Yu G., Yuan S.,  
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Arabidopsis ORF clones";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC005397; AAC62893.1; -;  
DR EMBL: BT004820; AAC44086.1; -;  
DR PIR: H84898; H84898.  
DR GO: GO:0003864; F3-methyl-2-oxobutanate hydroxymethyltransf. . .; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0015940; P:pantothenate biosynthesis; IEA.  
DR InterPro: IPR003700; Pantoate transf.  
DR Pfam: PF02548; Pantoate transf; 1.  
DR TIGRfams: TIGR00222; panB; 1.  
KW Transferase.  
SQ SEQUENCE 347 AA; 36693 MW; 1A37916DA6B97795 CRC64;  
Query Match 35.3%; Score 476.5; DB 10; Length 347;  
Best Local Similarity 39.9%; Pred. No. 2.3e-29;  
Matches 107; Conservative 48; Mismatches 102; Indels 11; Gaps 7;  
QY 4 TTISLLQKYKQDKRFATITAYDYSFAKLFADGELNVLVGDLSGMTVQGHDSLPTVVA 63  
DB 43 TLTHLRQKHRRGP-ITVVTADYPSAVHLDTAGIDVCLVGDSSMNVVGHDTLPISLD 101  
QY 64 DIAYHTAAVRGAPNCLLADLPFMAY-ATPEQAFENAAATVNR-AGANMVKEGE-WLV 120  
DB 102 EMLVHCRAVARGAKRPLLVGDLPPFGTYESSSSQAVDTAVRVLKEGMDAILEGGSASRI 161  
QY 121 ETVMQLTERAVFCVCHLGLTPQSVNIFGGYKVGQRDEAGDQLLSDALALEAAGQLVL 180  
DB 162 TAAKAIVEAGIAGVGHVGLTPQAISVLGGFRFGGRNIASAVKVVETAMALQEGCFSVVL 221  
QY 181 ECVPVLEAKRITBALAIPVIGAGNVTDGQILVMDHAFGIT-----GCHIPKFAKNFLA 235  
DB 222 ECVPPPVAARATGALKIPIGIGAGFCGSGQVLVYHDLGMMQHPHAKVTPKCKQY-A 280  
QY 236 ETGD-IRAAVRQMAEVESGVYPEGHS 262  
DB 281 NVGEVINKALMEYKEVKVFPGPSHS 308

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OM protein - protein search, using sw model

Run on: July 29, 2004, 10:26:56 ; Search time 53 Seconds  
(without alignments)  
1407.406 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 1349

Sequence: 1 MKPTTISLLQYKQDKKRPFA.....RQYMAVESGVVPGHEHSPH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Genesep29Jan04:\*  
1: Genesep1980s:\*  
2: Genesep1990s:\*  
3: Genesep2000s:\*  
4: Genesep2001s:\*  
5: Genesep2002s:\*  
6: Genesep2003as:\*  
7: Genesep2003bs:\*  
8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1345	99.7	264	AAU34445	AAU34445 E. coli c
2	1345	99.7	264	ABU28494	ABU28494 Protein e
3	1322	98.0	264	AAU14820	AAU14820 PanB amin
4	1243.5	92.2	264	ABU48131	ABU48131 Protein e
5	1237.5	91.7	269	AAU38309	AAU38309 Salmonell
6	1231.5	91.3	263	ABU28136	ABU28136 Protein e
7	1210	89.7	264	AAU26016	AAU26016 Escherich
8	1204.5	89.3	263	ABU36114	ABU36114 Klebsiell
9	1204.5	89.3	263	ABU32246	ABU32246 Protein e
10	1074	79.6	263	ABU45584	ABU45584 Protein e
11	1063.5	78.8	266	ABU49943	ABU49943 Protein e
12	968.5	71.8	263	ABU40865	ABU40865 Protein e
13	955.5	70.8	264	ABU67584	ABU67584 Phototrab
14	950	70.4	264	ABU49170	ABU49170 Protein e
15	795.5	59.0	280	ABU40160	ABU40160 Protein e
16	784.5	58.2	267	AAU26017	AAU26017 Schizosac
17	745.5	55.3	266	ABU41992	ABU41992 Protein e
18	726	53.8	263	ABU37938	ABU37938 Protein e
19	726	53.8	269	ABU17292	ABU17292 Protein e
20	726	53.8	284	ADA36659	ADA36659 Acinetoba
21	723	53.6	263	ABP78435	ABP78435 N. gonorr
22	723	53.6	263	ABU37337	ABU37337 Protein e
23	719	53.3	271	ABU21403	ABU21403 Protein e
24	713	52.9	271	ABU19911	ABU19911 Protein e
25	709	52.6	271	ABU22794	ABU22794 Protein e

ABU06070 N. mening  
ABU35143 Protein e  
AAU36454 Pseudomon  
ABU38792 Protein e  
AAU1244 B. subtil  
ABU25007 Protein e  
ABU24616 Protein e  
ABU17749 Protein e  
AAU35249 Enterococ  
ABU29017 Protein e  
ABU29684 Protein e  
ADC94386 E. faeciu  
ABU4829 Protein e  
ABU36755 Protein e  
ABU4006 Protein e  
ABU34020 Protein e  
ABU26352 Protein e  
ABU35977 Protein e  
ABU48006 Listeria  
ABU32785 Protein e

## ALIGNMENTS

### RESULT 1

AAU34445  
ID AAU34445 standard; protein; 264 AA.

AC AAU34445;

DT 14-FEB-2002 (first entry)

DE E. coli cellular proliferation protein #26.

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;  
antibacterial; drug design.

OS Escherichia coli.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257911P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JB, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS52304.

XX New polynucleotides for the identification and development of  
antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; SEQ ID NO 10038; 51pp; English.

CC The invention relates to antisense inhibitors of genes essential to  
prokaryotic cellular proliferation, their use in identifying the genes,  
their use in the discovery of novel antibiotics, the essential genes  
themselves and the encoded proteins. The prokaryotes used are Escherichia  
coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence represents an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 4; Length 264;  
Best Local Similarity 99.6%; Pred. No. 4.2e-131;  
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60  
DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60  
QY 61 TVADIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANMVKIEGSEWLV 120  
DB 61 TVADIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANMVKIEGSEWLV 120  
QY 121 ETVMQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180  
DB 121 ETVMQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180  
QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
DB 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
QY 241 RAAVQYMAEVESGVYPGEEHSFH 264  
DB 241 RAAVQYMAEVESGVYPGEEHSFH 264

RESULT 2  
ABU28494  
ID ABU28494 standard; protein; 264 AA.

XX AC ABU28494;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #14021.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Escherichia coli.  
XX EN W0200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US0009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX DR WPI; 2003-029926/02.  
XX DR N-PSDB; ACA32364.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 56418; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the patent prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 6; Length 264;  
Best Local Similarity 99.6%; Pred. No. 4.2e-131;  
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60  
DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60  
QY 61 TVADIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANMVKIEGSEWLV 120  
DB 61 TVADIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANMVKIEGSEWLV 120  
QY 121 ETVMQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180  
DB 121 ETVMQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180  
QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
DB 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240  
QY 241 RAAVQYMAEVESGVYPGEEHSFH 264  
DB 241 RAAVQYMAEVESGVYPGEEHSFH 264

RESULT 3  
AAV14820  
ID AAV14820 standard; protein; 264 AA.  
XX AC AAV14820;  
XX DT 29-OCT-1999 (first entry)

X PanB amino acid sequence.  
E  
X  
X Pantothenic acid-requiring complementary gene; yeast; gene marker;  
W recombinant microorganism production.  
X  
S Unidentified.  
S  
N JPL1215986-A.  
N  
X 10-AUG-1999.  
D  
X 23-JAN-1998; 98JP-00025194.  
F  
X 23-JAN-1998; 98JP-00025194.  
R  
X (KOKU-) KOKUZEI CHO CHOHAN.  
A  
X WPI; 1999-511114/43.  
R  
X Pantothenic acid-requiring complementary gene - used to produce  
T recombinant microorganisms.  
T  
X Disclosure; Fig 4; 8pp; Japanese.  
S  
C The invention relates to a pantothenic acid-requiring complementary yeast  
C gene. The invention provides a method for the selection of a transformed  
C microbe in which a gene marker containing the above DNA is used and the  
C selection is carried out by phenotyping the gene, and a transformed  
C microbe is selected. The gene can be used to produce recombinant  
C microorganisms. The present sequence represents a panB amino acid  
C sequence  
X  
X  
Q Sequence 264 AA;  
  
Query Match 98.0%; Score 1322; DB 2; Length 264;  
Best Local Similarity 98.1%; Pred. No. 1e-128;  
Matches 259; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
1 MKPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGLSLGTVQGHSTLPLV 60  
1 MKPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGLSLGTVQGHSTLPLV 60  
  
61 TVADIAHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANNVKEGGWLV 120  
61 TVEDIAHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANNVKEGGWLV 120  
  
121 ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGQLLVL 180  
121 ETVRMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGQLLVL 180  
  
181 ECVPELAKRITELALPVGIGAGNVTDGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 240  
181 ECVPELAKRITELALPVGIGAGNVTDGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 240  
  
241 RAAVRQYMAEVESGVYGEHSFH 264  
241 RAAVRQYMAEVESGVYGEHSFH 264

XX WO200277183-A2.  
XX  
XX 03-OCT-2002.  
XX  
XX 21-MAR-2002; 2002WO-US009107.  
XX  
XX 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
XX 25-OCT-2001; 2001US-0342923P.  
XX 08-FEB-2002; 2002US-00072851.  
XX 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA52001.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 76055; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism's activity; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the  
XX proliferation of an organism. The antisense nucleic acids are useful for  
XX identifying proteins or screening for homologous nucleic acids required  
XX for cellular proliferation to isolate candidate molecules for rational  
XX drug discovery programs, or for screening homologous nucleic acids  
XX required for proliferation in cells other than S. aureus, S. typhimurium,  
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
XX the target prokaryotic essential genes. Note: The sequence data for this  
XX patent did not form part of the printed specification, but was obtained  
XX in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 264 AA;  
  
Query Match 92.2%; Score 1243.5; DB 6; Length 264;  
Best Local Similarity 91.8%; Pred. No. 1.5e-120;  
Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;  
  
QY 2 KPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGLSLGTVQGHSTLPLV 61  
DB 3 KPTTIAVLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGLSLGTVQGHSTLPLV 62  
  
QY 62 VADIAHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANNVKEGGWLV 121  
DB 63 VEDIAHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANNVKEGGWLV 122

QY 122 TVQMLTERAVPVCGHGLTPOSVNIFGGYKVOGRDEAGDQLSDALAEAGQALLVLE 181  
 DB 123 TVKMLTERAVPVCGHGLTPOSVNIFGGYKVOGRDEAGDQLSDALAEAGQALLVLE 181  
 QY 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDIR 241  
 DB 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDIR 241  
 QY 242 AAVRQYMAEVESGVYPGEHSFH 264  
 DB 242 AAVRQYMAEVESGVYPGEHSFH 264

RESULT 5  
 AAU38309  
 ID AAU38309 standard; protein; 269 AA.  
 AC AAU38309;  
 XX 14-FEB-2002 (first entry)  
 DT Salmonella typhi cellular proliferation protein #200.  
 DE Antisense; prokaryotic cellular proliferation protein; antibiotic;  
 KW antibacterial; drug design.  
 KW Salmonella typhi.  
 OS WO200170955-A2.  
 PN 27-SEP-2001.  
 PD 21-MAR-2001; 2001WO-US009180.  
 PF 21-MAR-2000; 2000US-0191078P.  
 PR 23-MAY-2000; 2000US-0206848P.  
 PR 26-MAY-2000; 2000US-0207727P.  
 PR 23-OCT-2000; 2000US-0242578P.  
 PR 27-NOV-2000; 2000US-0253625P.  
 PR 22-DEC-2000; 2000US-0257531P.  
 PR 16-FEB-2001; 2001US-0269308P.  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
 PI Yamamoto RT, Xu HH;  
 XX WPI; 2001-611495/70.  
 DR N-PSDB; AAS56168.

XX New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids.  
 XX Example 3; SEQ ID NO 13902; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to, to express these proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence represents an essential prokaryotic  
 CC cellular proliferation protein. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 269 AA;  
 SQ Query Match 91.7%; Score 1237.5; DB 4; Length 269;  
 Best Local Similarity 91.3%; Pred. No. 6.4e-120;  
 Matches 240; Conservative 12; Mismatches 10; Indels 1; Gaps 1;  
 QY 2 KPTTISLQKQKQKREATTAYDSYFAKLPADEGNVLMVGDLSLGMTVQGHDSLTPVT 61  
 DB 8 KPTTIAVLQKQKQKREATTAYDSYFAKLPADEGNVLMVGDLSLGMTVQGHDSLTPVT 67  
 QY 62 VADIAHTAAVERGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANVWKIEGGEWLVE 121  
 DB 68 VEDIAHTRAVRGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANVWKIEGGAWLVD 127  
 QY 122 TVQMLTERAVPVCGHGLTPOSVNIFGGYKVOGRDEAGDQLSDALAEAGQALLVLE 181  
 DB 128 TVKMLTERAVPVCGHGLTPOSVNIFGGYKVOGRDEAGDQLSDALAEAGQALLVLE 186  
 QY 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDIR 241  
 DB 187 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDIR 246  
 QY 242 AAVRQYMAEVESGVYPGEHSFH 264  
 DB 247 AAVRQYMAEVESGVYPGEHSFH 269

RESULT 6  
 ABU28136  
 ID ABU28136 standard; protein; 263 AA.  
 AC ABU28136;  
 XX 19-JUN-2003 (first entry)  
 DT Protein encoded by Prokaryotic essential gene #13663.  
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 KW Enterobacter cloacae.  
 OS WO200277193-A2.  
 PN 03-OCT-2002.  
 PD 21-MAR-2002; 2002WO-US009107.  
 PF 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA32006.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids, required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX Claim 25; SEQ ID NO 56060; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense



XX PS Disclosure; Fig 5; 367pp; English.

XX CC The invention relates to a crystal of ketopantoate

XX CC hydroxymethyltransferase (KPHMT), including crystals of selenium atom

XX CC KPHMT derivatives. The KPHMT crystal has the monoclinic point group 2,

XX CC space group P2<sub>1</sub> and the 3-dimensional atomic co-ordinates given in the

XX CC specification. KPHMT crystal diffracts X-rays for the detection of atomic

XX CC co-ordinates of KPHMT to a resolution of better than 2 Angstroms. The

XX CC KPHMT crystal is useful in a computer-based method of rational drug

XX CC design, for determining 3D structures of KPHMT homologues or analogues of

XX CC unknown structure, for determining the structure of a protein, for

XX CC determining the structure of a compound bound to KPHMT, or for assessing

XX CC the ability of a candidate modulator to interact with KPHMT. The KPHMT

XX CC crystal is also useful for designing, screening, identifying and

XX CC developing KPHMT inhibitor compounds, or to solve the crystal structure

XX CC of proteins, such as KPHMT-ligand complexes, KPHMT chimeric-ligand

XX CC complexes or KPHMT homologues or analogues of unknown structure. The

XX CC KPHMT inhibitor is useful for inhibiting KPHMT activity, and in the

XX CC manufacture of a medicament for treating diseases such as microbial

XX CC infection. This sequence represents an Escherichia coli secondary

XX CC structure protein relating to the KPHMT family proteins of the invention

XX CC Sequence 264 AA;

Query Match 89.7%; Score 1210; DB 6; Length 264;

Best Local Similarity 91.7%; Pred. No. 4.5e-117;

Matches 242; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKPTTISLLQKYQDKKRPATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSXLPV 60

Db 1 MKPTTISLLQKYQDKKRPATITAYDYSFAKLFADEGLNVLVXXLGMTVQGHDSXLPV 60

QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENATVMRAGANWVKIEGSEWLV 120

Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENATVMRAGANWVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQLLV 180

Db 121 ETVQMLTERAVPVCGKXLTXXSVNIFXGYKVGQGRDEAGDQLLSDALALEAAGQLLV 180

QY 181 ECVPELAKRITALEAIPVIGAGNVTGQILVMDHDAFGITGGHIPKFNFLAETGDI 240

Db 181 XCVPELXKRITALEAIPVIGXAGNVTGKILXWHXAFITGGHIPKFNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264

Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 8

AAU36114

ID AAU36114 standard; protein; 263 AA.

XX AC AAU36114;

XX 14-FEB-2002 (first entry)

XX Klebsiella pneumoniae cellular proliferation protein #102.

XX Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX antibacterial; drug design.

XX Klebsiella pneumoniae.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS533973.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; SEQ ID NO 11707; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the genes,

CC themselves and the encoded proteins. The prokaryotes used are Escherichia

CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,

CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic

CC development. The antisense nucleic acids can also be used to identify

CC proteins used in proliferation, to express these proteins, and to obtain

CC antibodies capable of binding to the expressed proteins. The proteins can

CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous

CC nucleic acids which are required for cell proliferation in a wide variety

CC of organisms. The present sequence represents an essential prokaryotic

CC cellular proliferation protein. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 263 AA;

Query Match 89.3%; Score 1204.5; DB 4; Length 263;

Best Local Similarity 89.0%; Pred. No. 1.7e-116;

Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKPTTISLLQKYQDKKRPATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSXLPV 60

Db 1 MKPTTISLLQKYQDKKRPATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSXLPV 60

QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENATVMRAGANWVKIEGSEWLV 120

Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENATVMRAGANWVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQLLV 180

Db 121 DTVERLAERAVPVCGHLGTPQSVNIFGGYKVGQGRD-AAQTLFEDALALEAAGQLLV 179

QY 181 ECVPELAKRITALEAIPVIGAGNVTGQILVMDHDAFGITGGHIPKFNFLAETGDI 240

Db 180 ECVPELAKRITALEAIPVIGAGNVTGQILVMDHDAFGITGGHIPKFNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264

Db 240 RAAVRQYMAEVESGVYPGEHSFH 263

RESULT 9

ABU32246

ID ABU32246 standard; protein; 263 AA.

XX AC ABU32246;

XX 19-JUN-2003 (first entry)



JE Protein encoded by Prokaryotic essential gene #17773.  
 CX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 CW Klebsiella pneumoniae.  
 CS WO200277183-A2.  
 CN 03-OCT-2002.  
 PD 21-MAR-2002; 2002WO-US009107.  
 PE 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 CX (ELIT-) ELITRA PHARM INC.  
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
 PI WPI; 2003-029926/02.  
 JR N-PSDB; ACA36116.  
 CX New antisense nucleic acids, useful for identifying proteins or screening  
 CX for homologous nucleic acids required for cellular proliferation to  
 CX isolate candidate molecules for rational drug discovery programs.  
 CX Claim 25; SEQ ID NO 60170; 1766pp; English.  
 CX The invention relates to an isolated nucleic acid comprising any one of  
 CX the 6213 antisense sequences given in the specification where expression  
 CX of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CX (1) a vector comprising a promoter operably linked to the nucleic acid  
 CX encoding a polypeptide whose expression is inhibited by the antisense  
 CX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CX polypeptide or its fragment whose expression is inhibited by the  
 CX antisense nucleic acid; (4) an antibody capable of specifically binding  
 CX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CX proliferation or the activity of a gene in an operon required for  
 CX proliferation; (7) identifying a compound that influences the activity of  
 CX the gene product or that has an activity against a biological pathway  
 CX required for proliferation, or that inhibits cellular proliferation; (8)  
 CX identifying a gene required for cellular proliferation or the biological  
 CX pathway in which a proliferation-required gene or its gene product lies  
 CX or a gene on which the test compound that inhibits proliferation of an  
 CX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CX compound's activity; (11) a culture comprising strains in which the gene  
 CX product is overexpressed or underexpressed; (12) determining the extent  
 CX to which each of the strains is present in a culture or collection of  
 CX strains; or (13) identifying the target of a compound that inhibits the  
 CX proliferation of an organism. The antisense nucleic acids are useful for  
 CX identifying proteins or screening for homologous nucleic acids required  
 CX for cellular proliferation to isolate candidate molecules for rational  
 CX drug discovery programs, or for screening homologous nucleic acids  
 CX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CX the target prokaryotic essential genes. Note: The sequence data for this  
 CX patent did not form part of the printed specification, but was obtained  
 CX in electronic format directly from WIPO at  
 CX ftp.wipo.int/pub/published\_pct\_sequences  
 CX Sequence 263 AA;  
 CX  
 CX Query Match 89.3%; Score 1204.5; DB 6; Length 263;  
 CX Best Local Similarity 89.0%; Pred. No. 1.7e-116;  
 CX Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;  
 CX  
 CX 1 MKPTTISLQYKQDKRFAITAYDSFAKLFADEGINVLMVGDLSIGMTVQGHSTLFPV 60  
 CX  
 CX 1 MKPTTIALQKCKEKEFAITAYDSFAKLFADEGINVLLVGDLSIGMTVQGHSTLFPV 60

QY 61 TVADIAYHTAAVRGAPNCILLADLPFMAYATPEQAFENAAATVMEAGANNVKEGEMLV 120  
 DB 61 TVEDIAYHTAAVRGAPNSULLADLPFMAYATPEQTFAAAIIVMRAGANNVKEGAWLA 120  
 QY 121 ETYQMLTERAVPVCGHLGLTPQSVNIFGGYKVGQGRDEAGDOLLSALAEAGQLLV 180  
 DB 121 DTVMLAERAVPVCGHLGLTPQSVNIFGGYKVGQGRD-AAQTLFEDALAEAGQLLV 179  
 QY 181 ECVPELAKRITDALTPVIGAGNVTDGQILVMDHAFGTTGGHIPKFAKNFLAETGSI 240  
 DB 180 ECVPELAKRITDALTPVIGAGNVTDGQILVMDHAFGTTGGHIPKFAKNFLAETGSI 239  
 QY 241 RAAVRQYIAEVESGVYPGEHSHF 264  
 DB 240 RAAVRQYIAEVESGVYPGEHSHF 263  
 RESULT 10  
 ABU45584  
 ID ABU45584 standard; protein; 263 AA.  
 AC ABU45584;  
 CX 19-JUN-2003 (first entry)  
 CX Protein encoded by Prokaryotic essential gene #31111.  
 CX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 CX Salmonella paratyphi.  
 CX WO200277183-A2.  
 CX 03-OCT-2002.  
 CX 21-MAR-2002; 2002WO-US009107.  
 CX 21-MAR-2001; 2001US-00815242.  
 CX 06-SEP-2001; 2001US-00948993.  
 CX 25-OCT-2001; 2001US-0342923P.  
 CX 08-FEB-2002; 2002US-00072851.  
 CX 06-MAR-2002; 2002US-0362699P.  
 CX (ELIT-) ELITRA PHARM INC.  
 CX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 CX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
 CX WPI; 2003-029926/02.  
 CX N-PSDB; ACA49454.  
 CX New antisense nucleic acids, useful for identifying proteins or screening  
 CX for homologous nucleic acids required for cellular proliferation to  
 CX isolate candidate molecules for rational drug discovery programs.  
 CX Claim 25; SEQ ID NO 73508; 1766pp; English.  
 CX The invention relates to an isolated nucleic acid comprising any one of  
 CX the 6213 antisense sequences given in the specification where expression  
 CX of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CX (1) a vector comprising a promoter operably linked to the nucleic acid  
 CX encoding a polypeptide whose expression is inhibited by the antisense  
 CX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CX polypeptide or its fragment whose expression is inhibited by the  
 CX antisense nucleic acid; (4) an antibody capable of specifically binding  
 CX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CX proliferation or the activity of a gene in an operon required for  
 CX proliferation; (7) identifying a compound that influences the activity of  
 CX the gene product or that has an activity against a biological pathway  
 CX required for proliferation, or that inhibits cellular proliferation; (8)  
 CX identifying a gene required for cellular proliferation or the biological  
 CX pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 263 AA;

Query Match 79.6%; Score 1074; DB 6; Length 263;  
 Best Local Similarity 81.4%; Pred. No. 6.1e-103;  
 Matches 215; Conservative 13; Mismatches 34; Indels 2; Gaps 2;  
 QY 1 MKPTTISLQKVKODKRRATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHDSLTPV 60  
 DB 2 MKPTTISLQKVKODKRRATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHDSLTPV 60  
 QY 61 TVADIAHYHTAAVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMKIEGGSLV 120  
 DB 61 TVEDIAHYRLXTRGAPNCLLLSDLPFFCTPTPEQACENAAIVVRAGANVMKIERGALV 120  
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNIFFGYKVQGRDAGDQLLSDALALEAAGALLVL 180  
 DB 121 DTVKMLTERACPCGHXLRHQSVNIFGYKIQGRA-TFGRVLLDDALALEAPALNCLV 179  
 QY 181 ECVPVELAKRITEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 240  
 BB 180 ECVPVELAKRITEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 239  
 QY 241 RAAVRQYMAEVESGVYPGEHSFH 264  
 DB 240 RAAVRQYMAEVESGVYPGEHSFH 263

RESULT 11  
 ABU49943  
 ID ABU49943 standard; protein; 266 AA.

XX AC ABU49943;  
 XX DT 19-JUN-2003 (first entry)  
 XX DE Protein encoded by Prokaryotic essential gene #35470.  
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX OS *Yersinia pestis*.  
 XX FN WO200277183-A2.  
 XX PD 03-OCT-2002.  
 XX XX 21-MAR-2002; 2002WO-US009107.  
 XX PR 21-MAR-2001; 2001US-00815242.  
 XX PR 06-SEP-2001; 2001US-00948993.  
 XX PR 25-OCT-2001; 2001US-0342923P.  
 XX PR 08-FEB-2002; 2002US-00072851.  
 XX PR 06-MAR-2002; 2002US-0362699P.  
 XX PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA53813.  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 77867; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 266 AA;

Query Match 78.8%; Score 1063.5; DB 6; Length 266;  
 Best Local Similarity 76.1%; Pred. No. 7.6e-102;  
 Matches 201; Conservative 36; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 MKPTTISLQKVKODKRRATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHDSLTPV 60  
 DB 2 MKPTTISLQKVKODKRRATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHDSLTPV 61  
 QY 61 TVADIAHYHTAAVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMKIEGGSLV 120  
 DB 62 TVADMAHYHTAAVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMKIEGGSLV 121  
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNIFFGYKVQGRDAGDQLLSDALALEAAGALLVL 180  
 DB 122 DTRMLAERAVPCVGHGLTPOSVNIFFGYKVQGRDAGDQLLSDALALEAAGALLVL 181  
 QY 181 ECVPVELAKRITEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 239  
 DB 182 ECVPVELAKRITEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 241  
 QY 240 RAAVRQYMAEVESGVYPGEHSFH 263  
 DB 242 RAAVRQYMAEVESGVYPGEHSFH 265

RESULT 12  
 ABU40865  
 ID ABU40865 standard; protein; 263 AA.

ABU40865;  
19-JUN-2003 (first entry)  
Protein encoded by Prokaryotic essential gene #26392.  
Antisense; prokaryotic essential gene; cell proliferation; drug design.  
Proteus sp.  
WO200277183-A2.  
03-OCT-2002.  
21-MAR-2002; 2002WO-US009107.  
21-MAR-2001; 2001US-00815242.  
06-SEP-2001; 2001US-00948993.  
25-OCT-2001; 2001US-0342923P.  
08-FEB-2002; 2002US-00072851.  
06-MAR-2002; 2002US-0362699P.  
(ELIT-) ELITRA PHARM INC.  
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
WPI; 2003-029926/02.  
N-PSDB; ACA44735.  
New antisense nucleic acids, useful for identifying proteins or screening  
for homologous nucleic acids required for cellular proliferation to  
isolate candidate molecules for rational drug discovery programs.  
Claim 25; SEQ ID NO 68789; 1766pp; English.  
The invention relates to an isolated nucleic acid comprising any one of  
the 6213 antisense sequences given in the specification where expression  
of the nucleic acid inhibits proliferation of a cell. Also included are:  
(1) a vector comprising a promoter operably linked to the nucleic acid  
encoding a polypeptide whose expression is inhibited by the antisense  
nucleic acid; (2) a host cell containing the vector; (3) an isolated  
polypeptide or its fragment whose expression is inhibited by the  
antisense nucleic acid; (4) an antibody capable of specifically binding  
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
proliferation or the activity of a gene in an operon required for  
proliferation; (7) identifying a compound that influences the activity of  
the gene product or that has an activity against a biological pathway  
required for proliferation, or that inhibits cellular proliferation; (8)  
identifying a gene required for cellular proliferation or the biological  
pathway in which a proliferation-required gene or its gene product lies  
or a gene on which the test compound that inhibits proliferation of an  
organism acts; (9) manufacturing an antibiotic; (10) profiling a  
compound's activity; (11) a culture comprising strains in which the gene  
product is overexpressed or underexpressed; (12) determining the extent  
to which each of the strains is present in a culture or collection of  
strains; or (13) identifying the target of a compound that inhibits the  
proliferation of an organism. The antisense nucleic acids are useful for  
identifying proteins or screening for homologous nucleic acids required  
for cellular proliferation to isolate candidate molecules for rational  
drug discovery programs, or for screening homologous nucleic acids  
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
the target prokaryotic essential genes. Note: The sequence data for this  
patent did not form part of the printed specification, but was obtained  
in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences  
Sequence 263 AA;  
Query Match 71.8%; Score 968.5; DB 6; Length 263;  
Best Local Similarity 70.8%; Pred. No. 5.6e-92;

Matches	187;	Conservative	33;	Mismatches	43;	Indels	1;	Caps	
Qy	1	MKPTTISLLQKYKDQKKRFAITITAYDYSFAKLFADEGLNVLVGDSLGTMVQGHSTLPV	60						
Db	1	MKPVTLSLNRYYQEKKKFAITITAYDASFARLFANEGIPAMLTIGDSLGMTLQGHDSLPV	60						
Qy	61	TVADTAYHTAAVRGAPNCILLADLPWAYATPEAFENAAATVMRAGANNVKIEGGEWLV	120						
Db	61	TVEQYATYHTRCVRGAPNAFLIAMPFMSYSTPEQACLNAAILMQAGANNVKIEGGSWLI	120						
Qy	121	ETVQMLTERAVPVCCHLGUTPQSNIIFGGYKVQGRGDEAGDQLLSDALALEAAGAQLLV	180						
Db	121	PIVKM.LTERAVPVCIHGLGTQSVNVFGGYKVQGEEAAAEQLKQDAWALEAAGAQLVL	180						
Qy	181	ECVPVELAKRITEALAIPIVGIGAGNVTDGOILVMDPAFIGTGTHPKFAKNFLAETGDI	240						
Db	181	ECVPSVAKTITGNSINIFVIGIGAGNVTDGOILVMHDLLGLT-PNAPKFSKNFLQEAGSL	239						
Qy	241	RAARQYMAEVESGVYPGEHSFH	264						
Db	240	PEAVRLYQQVEQKLFPQEQHSFN	263						
RESULT	13								
ID	ABM67584								
ABM67584	standard; protein; 264 AA.								
XX	ABM67584;								
XX	20-NOV-2003 (first entry)								
DT	Photorhabdus luminescens protein sequence #681.								
DE									
KW	Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;								
KW	detection; food; gene expression; plant; animal; microorganism; toxin;								
KW	antibiotic; biopesticide; virulence factor; disease model; plague;								
KW	whooping cough.								
XX	Photorhabdus luminescens.								
OS	WC200294867-A2.								
PN	28-NOV-2002.								
PD	07-FEB-2002; 2002WO-IB003040.								
XX	07-FEB-2001; 2001PR-00001659.								
PF	(INSP ) INST PASTEUR.								
XX	(CNRS ) CNRS CENT NAT RECH SCI.								
PA	Duchaud E, Tacurit S, Glaser P, Frangeul L, Kunst F, Danchin A;								
PA	Buchrieser C;								
PI	WPI; 2003-148459/14.								
DR	Genomic sequence of Photorhabdus luminescens and encoded polypeptides,								
XX	useful e.g. as therapeutic antimicrobials and agricultural pesticides.								
PS	Claim 2; SEQ ID NO 681; 1205bp; French.								
CC	The invention relates to the isolation of genes and their encoded								
CC	proteins from Photorhabdus luminescens. The isolated sequences are								
CC	sources of probes and primers for detecting the genome of P. luminescens								
CC	and related species; to study polymorphisms, for gene analysis and for								
CC	detection/amplification of the genes. Antibodies (Ab) raised against the								
CC	polypeptides encoded by the genes are used for detection/identification								
CC	P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that								
CC	carry a gene-containing vector are used to select compounds that								
CC	modulate, regulate, induce or inhibit expression of the genes in plants,								
CC	animals or microorganisms other than P. luminescens and are able to alter								
CC	response or sensitivity to toxins and antibiotics produced by P.								
CC	luminescens. Cells transformed to express the genes are useful for								

Query Match	71.8%;	Score 968.5;	DB 6;	Length 263;
Best Local Similarity	70.8%;	Pred. No. 5.6e-92;		

CC recombinant production of the proteins, particularly toxins and  
 CC antibacterials useful as insecticides, bactericides and fungicides. The  
 CC genes, proteins, vectors containing the genes and Ab are also useful  
 CC therapeutically (to treat microbial infection by bacteria or fungi that  
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
 CC biopesticides. Other uses of the genes and the proteins are as virulence  
 CC factors and for identifying targets of human diseases for which P.  
 CC luminescens is a model (particularly plague and whooping cough). This  
 CC sequence represents one of the isolated P. luminescens proteins  
 XX  
 SQ Sequence 264 AA;  
 Query Match 70.8%; Score 955.5; DB 6; Length 264;  
 Best Local Similarity 68.6%; Pred. No. 1.3e-90;  
 Matches 181; Conservative 38; Mismatches 44; Indels 1; Gaps 1;  
 QY 1 MKPTTISLLQKQKRRPATITAYDYSFAKLFADEGLNMLVGSLSGMTVQGHSTLTPV 60  
 DB 1 MKPMTITDLNQLKKRKEPATITAYDASFAHLFABQGDVMDLVGDSLSGMTVQGHSTLTPV 60  
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVMRAGANNVKIEGSEWLV 120  
 DB 61 TVEDIVYHTRCVRAGPYTTFIADMPFMSYATPEQSCENAAKLMRAGANNVKIEGSEWLV 120  
 QY 121 ETVQMLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLSDALALEAAGALLVL 180  
 DB 121 DTINMLTERSVPVCAHLGLTPQSVHILGGYKVGQGRDEVSAANQLIKDAITLLEKAGIQLLVL 180  
 QY 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 239  
 QY 241 RAAVROYMAEVESGVYPGEHSFH 264  
 DB 240 RDAIRLYKEQVESGIYPGEHSFY 263

RESULT 14  
 ABU49170  
 ID ABU49170 standard; protein; 264 AA.  
 AC ABU49170;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #34697.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Vibrio cholerae.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA53040.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.  
 XX Claim 25; SEQ ID NO 77094; 1766pp; English.  
 XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than S. aureus, S. typhimurium,  
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 264 AA;  
 Query Match 70.4%; Score 950; DB 6; Length 264;  
 Best Local Similarity 68.7%; Pred. No. 4.7e-90;  
 Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;  
 QY 1 MKPTTISLLQKQKRRPATITAYDYSFAKLFADEGLNMLVGSLSGMTVQGHSTLTPV 60  
 DB 1 MKKITINDLMKQKGRKFATSTAYDASFAQLPFESQEMPVLLVGSLSGMTVQGHSTLTPV 60  
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVMRAGANNVKIEGSEWLV 120  
 DB 61 TVDDIAYHTRCVRKGSFNCLLMADMPFMSYATPEQACENAAKLVAGANNVKIEGSEWLV 120  
 QY 121 ETVQMLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLSDALALEAAGALLVL 180  
 DB 121 DTVKMLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEADKADRVRLDALAQEAGIQLLVL 180  
 QY 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 240  
 DB 181 ECVPAELANRITQLDVPVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGDI 240  
 QY 241 RAAVROYMAEVESGVYPGEHS 262  
 DB 241 RQAVAKYIEDVASGAFFDLAHT 262  
 RESULT 15  
 ABU40160  
 ID ABU40160 standard; protein; 280 AA.  
 XX  
 AC ABU40160;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #25687.  
 XX

W Antisense; prokaryotic essential gene; cell proliferation; drug design.  
X Pseudomonas putida.  
X W0200277183-A2.  
X  
X 03-OCT-2002.  
X  
X 21-MAR-2002; 2002WO-US009107.  
X  
X 21-MAR-2001; 2001US-00815242.  
X 06-SEP-2001; 2001US-00948993.  
X 25-OCT-2001; 2001US-0342923P.  
X 08-FEB-2002; 2002US-00072851.  
X 06-MAR-2002; 2002US-0362699P.  
X  
X (ELIT-) ELITRA PHARM INC.  
X Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
X Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
X  
X WPI; 2003-029926/02.  
X N-PSDB; ACA44030.  
X  
X New antisense nucleic acids, useful for identifying proteins or screening  
X for homologous nucleic acids required for cellular proliferation to  
X isolate candidate molecules for rational drug discovery programs.  
X  
X Claim 25; SEQ ID NO 68084; 1766pp; English.  
X  
X The invention relates to an isolated nucleic acid comprising any one of  
X the 6213 antisense sequences given in the specification where expression  
X of the nucleic acid inhibits proliferation of a cell. Also included are:  
X (1) a vector comprising a promoter operably linked to the nucleic acid  
X encoding a polypeptide whose expression is inhibited by the antisense  
X nucleic acid; (2) a host cell containing the vector; (3) an isolated  
X polypeptide or its fragment whose expression is inhibited by the  
X antisense nucleic acid; (4) an antibody capable of specifically binding  
X the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
X proliferation or the activity of a gene in an operon required for  
X proliferation; (7) identifying a compound that influences the activity of  
X the gene product or that has an activity against a biological pathway  
X required for proliferation, or that inhibits cellular proliferation; (8)  
X identifying a gene required for cellular proliferation or the biological  
X pathway in which a proliferation-required gene or its gene product lies  
X or a gene on which the test compound that inhibits proliferation of an  
X organism acts; (9) manufacturing an antibiotic; (10) profiling a  
X compound's activity; (11) a culture comprising strains in which the gene  
X product is overexpressed or underexpressed; (12) determining the extent  
X to which each of the strains is present in a culture or collection of  
X strains; or (13) identifying the target of a compound that inhibits the  
X proliferation of an organism. The antisense nucleic acids are useful for  
X identifying proteins or screening for homologous nucleic acids required  
X for cellular proliferation to isolate candidate molecules for rational  
X drug discovery programs, or for screening homologous nucleic acids  
X required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
X *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
X the target prokaryotic essential genes. Note: The sequence data for this  
X patent did not form part of the printed specification, but was obtained  
X in electronic format directly from WIPO at  
X ftp.wipo.int/pub/published\_pct\_sequences  
X  
X Sequence 280 AA;  
X  
X Query Match 59.0%; Score 795.5; DB 6; Length 280;  
X Best Local Similarity 56.8%; Pred. No. 5.7e-74;  
X Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;  
X  
X 1 MKPTTISLQKXQKKRFTATYDYSEAKLFADEGLNMYLVGDSLSIGMTVOGHDSSTLPV 60  
X 15 MPEVTLTTLNGLKAKGKIKMTLCTYDFAKASQAGVEVLVGDLSLGMVLQGHDSSTLPV 74  
X  
X 61 TVADIATVHTAAVRRCAPNCLLLADLPFMAHATPEQAFANATVMRAGANNVKIEGGEWLV 120

Db 75 TTAEMAYHTASVKRGNDGALILTDLPFMAHATPEQAFANATVMRAGANNVKIEGAAWLA 134  
Qy 121 ETVOMLTERAVPVCGLGLTPOSVINIFGKYKQGRDEAGDQLLSDALALAEAGQALLVL 180  
Db 135 ETIRLLAERGVPVCAHMGTLPTQTVNLGGYKVGQROEAQAFQMRADALALPQAGAAWLL 194  
Qy 181 ECPVVELAKRITTEALAIPIVIGAGNVTDGQILVNHDAFGIT-GGHIKPKAFKNFLAETGD 239  
Db 195 ECPVSELAAREITNAVGIPIVIGAGSATDGGVILVLDMLGLSLSGRVKPKVKNFMQGGPD 254  
Qy 240 IRAAVRQYMAEVESGVYPGEHSF 263  
Db 255 IHSALVAVYEAVKQVSPGSEHGF 278

Search completed: July 29, 2004, 10:33:17  
Job time : 55 secs



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WM protein - protein search, using sw model

Run on: July 29, 2004, 10:31:16 ; Search time 16 Seconds  
(without alignments)  
1587.160 Million cell updates/sec

Title: US-09-820-745-7  
Perfect score: 1349  
Sequence: 1 MKPTTISLLQKYQDKKRFA.....ROYMAEVSGVYPGEHSFH 264

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*

1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	1345	99.7	264	2	F64736
2	1296	96.1	264	2	B90646
3	1296	96.1	264	2	B85497
4	1243.5	92.2	264	2	AH0524
5	1063.5	78.8	266	2	AC0413
6	950	70.4	264	2	A82304
7	923.5	68.5	267	2	S55487
8	830	61.5	263	2	B84953
9	726	53.8	263	2	B81874
10	708	52.5	263	2	B81148
11	686.5	50.9	246	2	B82932
12	685.5	50.8	266	2	B83055
13	627	46.5	279	2	G83860
14	622	46.1	277	2	G69671
15	612	45.4	270	2	G72216
16	588.5	43.6	281	2	E70776
17	579.5	43.0	276	2	E97258
18	565.5	41.9	274	2	F81448
19	565.5	41.9	280	2	T50554
20	556.5	41.3	286	2	B87113
21	556	41.2	277	2	AF1684
22	549.5	40.7	291	2	T50565
23	546	40.5	277	2	AF1312
24	534	39.6	265	2	C70469
25	527.5	39.1	271	2	T47119
26	520.5	38.6	272	2	G90066
27	516	38.3	267	2	C90411
28	504.5	37.4	283	2	B71086
29	503.5	37.3	293	2	E75253

#### ALIGNMENTS

##### RESULT 1

F64736  
3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) - Escherichia coli (strain C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: F64736; A47152  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: F64736  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-264 <BLAT>  
A:Cross-references: GB:AE000122; GB:U00096; NID:91786315; PIDN:AACT7345.1; PID:91786326;  
A:Experimental source: strain K-12, substrain MG1655  
R:Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.  
J. Bacteriol. 175, 2125-2130, 1993  
A:Title: Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopant  
A:Reference number: A47152; MUID:93209959; PMID:8096212  
A:Accession: A47152  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6, 'AS', 9-11, 'C', 13-14, 'D', 16-62, 'E', 64-123, 'K', 125-264 <JON>  
A:Cross-references: GB:X65538; NID:G296058; PIDN:CAA46505.1; PID:G296059  
A:Experimental source: strain K12-82  
C:Genetics:  
A:Gene: panB  
C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase  
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 99.7%; Score 1345; DB 2; Length 264;  
Best Local Similarity 99.8%; Pred. No. 4.4e-98; Indels 0; Gaps 0;  
Matches 263; Conservative 1; Mismatches 0;

Qy	1	MKPTTISLLQKYQDKKRFAITAYDYSFAKLFADGLNMLVGLSGMTVGQHDSTLPV	60
Db	1	MKPTTISLLQKYQDKKRFAITAYDYSFAKLFADGLNMLVGLSGMTVGQHDSTLPV	60
Qy	61	TVADIATHTAATVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANVMKIEGWLIV	120
Db	61	TVADIATHTAATVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANVMKIEGWLIV	120
Qy	121	ETVQMLTERAVPVCGHGLTTPQSVNIFGGYKVGGRGDEAGDQLLSALALEAAGQLLV	180
Db	121	ETVQMLTERAVPVCGHGLTTPQSVNIFGGYKVGGRGDEAGDQLLSALALEAAGQLLV	180
Qy	181	ECVPVELAKRITETALAIPIVIGIGAGNVTDGQILVMHDAFGITGGHIPKPAKFLAETGDI	240
Db	181	ECVPVELAKRITETALAIPIVIGIGAGNVTDGQILVMHDAFGITGGHIPKPAKFLAETGDI	240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264  
 Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 2  
 B90646  
 hypothetical protein ECs0138 [imported] - Escherichia coli (strain O157:H7, substrain RIMD-0509952)  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
 C:Accession: B90646  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. et al. 2001. DNA Res. 8, 11-22, 2001.  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome organization.  
 A:Reference number: A95629; MUID:21156231; PMID:11258796  
 A:Accession: B90646  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-264 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA033561.1; PID:g13359594; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RIMD-0509952  
 C:Genetics:  
 A:Gene: ECs0138  
 C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 96.1%; Score 1296; DB 2; Length 264;  
 Best Local Similarity 95.8%; Pred. No. 3e-94;  
 Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKPTTISLLQYKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 60  
 Db 1 MKPTTISLLQYKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 60

QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120  
 Db 61 TVEDIAVHTAVRGAFCNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLSDALALEAQAQLLV 180  
 Db 121 ETVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEASDRLLSDALALEAQAQLLV 180

QY 181 ECVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 Db 181 ECVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264  
 Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 3  
 B85497  
 hypothetical protein panB [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: B85497  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew et al. 2001. Nature 409, 529-533, 2001.  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: B85497  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-264 <STO>  
 A:Cross-references: GB:AE005174; NID:g12512849; PIDN:AAG54438.1; GSPDB:GN00145; UWGP:201  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: panB  
 C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 96.1%; Score 1296; DB 2; Length 264;

Best Local Similarity 95.8%; Pred. No. 3e-94;  
 Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKPTTISLLQYKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 60  
 Db 1 MKPTTISLLQYKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 60

QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120  
 Db 61 TVEDIAVHTAVRGAFCNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLSDALALEAQAQLLV 180  
 Db 121 ETVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEASDRLLSDALALEAQAQLLV 180

QY 181 ECVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240  
 Db 181 ECVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264  
 Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 4  
 AH0524  
 3-methyl-2-oxobutanoate hydroxymethyltransferase [imported] - Salmonella enterica subsp. C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AH0524  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher et al. 2001. Nature 413, 848-852, 2001.  
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. et al. 2001. Nature 413, 848-852, 2001.  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi.  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AH0524  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-264 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD01336.1; PID:g16501464; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: STY0200  
 C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 92.2%; Score 1243.5; DB 2; Length 264;  
 Best Local Similarity 91.6%; Pred. No. 3.9e-90;  
 Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

QY 2 KPTTISLLQYKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 61  
 Db 3 KPTTIAVLQKQKPKFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHDSLPV 62

QY 62 VADIAVHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 121  
 Db 63 VEDIAVHTAVRGAFCNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 122

QY 122 TVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLSDALALEAQAQLLV 181  
 Db 123 TVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLSDALALEAQAQLLV 181

QY 182 CVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 241  
 Db 182 CVPVLEAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 241

QY 242 AAVRQYMAEVESGVYPGEHSFH 264  
 Db 242 AAVRQYMAEVESGVYPGEHSFH 264

RESULT 5



10413  
 -methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) [imported] - Yersinia pestis  
 ;Species: Yersinia pestis  
 ;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
 ;Accession: AC0413  
 ;Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
 ;Sho-faraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 ;I., M.; Rutherford, K.; Simmonds, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
 ;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 ;Reference number: AB0001; MUID:21470413; PMID:11586360  
 ;Accession: AC0413  
 ;Status: preliminary  
 ;Molecule type: DNA  
 ;Residues: 1-266 <NUP>  
 ;Cross-references: GB:AL590842; PIDN:CAC92631.1; PID:gl5981327; GSPDB:GN00175  
 ;Genetics:  
 ;Gene: panB  
 ;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase  
 ;Keywords: Coenzyme A biosynthesis; transferase

Query Match 78.8%; Score 1063.5; DB 2; Length 266;  
 Best Local Similarity 76.1%; Pred. No. 4.9e-76;  
 Matches 201; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

Y 1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHSTLPV 60  
 b 2 MKTTTMSQLRWKQKRRKFAITLTAAYDASFAQLFAEQGIQVLLVGDGLMTVQGHSTLPV 61

Y 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPQAFENATVVRAGANNVKIEGGWLV 120  
 b 62 TVADIAHTAAVRGAPNCLLLADLPMAVATPQAFENATVVRAGANNVKIEGGWLV 121

Y 121 ETVMQLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 180  
 b 122 DTIRMLAERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 181

Y 181 ECVPELAKRTEALAIPIVIGAGNVTGQILVMDAFGITGGHIPKPAKFLAETGD 239  
 b 182 ECVPELAKRTEALAIPIVIGAGNVTGQILVMDAFGITGGHIPKPAKFLAETGD 241

Y 240 IRAAVRQYMAEVESGVYPGEHSF 263  
 b 242 IRAALKVIEVEGGIYPAEHTF 265

RESULT 6  
 52304  
 -methyl-2-oxobutanate hydroxymethyltransferase VC0592 [imported] - Vibrio cholerae (sp  
 );Species: Vibrio cholerae  
 ;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 ;Accession: AB2304  
 ;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 ;Hardison, D.; Ermolaeva, M.B.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, F.  
 ;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 ;Reference number: AB2035; MUID:20406833; PMID:10952301  
 ;Accession: AB2304  
 ;Status: preliminary  
 ;Molecule type: DNA  
 ;Residues: 1-264 <HEI>  
 ;Cross-references: GB:AB004144; GB:AB003852; NID:99655017; PIDN:AAF93759.1; GSPDB:GN001  
 ;Experimental source: serogroup O1; strain N16961; biotype El Tor  
 ;Genetics:  
 ;Gene: VC0592  
 ;Map position: 1  
 ;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 70.4%; Score 950; DB 2; Length 264;  
 Best Local Similarity 68.7%; Pred. No. 3.7e-67;  
 Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

QY 1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHSTLPV 60  
 DB 1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHSTLPV 60

QY 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPQAFENATVVRAGANNVKIEGGWLV 120  
 DB 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPQAFENATVVRAGANNVKIEGGWLV 120

QY 121 ETVMQLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 180  
 DB 121 ETVMQLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 180

QY 181 ECVPELAKRTEALAIPIVIGAGNVTGQILVMDAFGITGGHIPKPAKFLAETGD 240  
 DB 181 ECVPELAKRTEALAIPIVIGAGNVTGQILVMDAFGITGGHIPKPAKFLAETGD 240

QY 241 IRAAVRQYMAEVESGVYPGEHSF 262  
 DB 241 IRAAVRQYMAEVESGVYPGEHSF 262

RESULT 7  
 S55487  
 probable 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) - fission yeast  
 N;Alternate names: protein AC5H10.09C  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-May-2000  
 C;Accession: S55487; T38973  
 R;Connor, R.; Churcher, C.M.  
 submitted to the EMBL Data Library, May 1995  
 A;Reference number: S55479  
 A;Accession: S55487  
 A;Molecule type: DNA  
 A;Residues: 1-267 <CON>  
 A;Cross-references: EMBL:Z49811; NID:9854599; PIDN:CAA89959.1; PID:9854608  
 R;Connor, R.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsen, S.V.  
 submitted to the EMBL Data Library, May 1995  
 A;Reference number: Z21821  
 A;Accession: T38973  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-267 <CO2>  
 A;Cross-references: EMBL:Z49811; PIDN:CAA89959.1; GSPDB:GN00066; SPDB:SPAC5H10.09C  
 A;Experimental source: strain 972h-; cosmid C5H10  
 C;Genetics:  
 A;Gene: SPDB:SPAC5H10.09C  
 A;Map position: 1  
 C;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase  
 C;Keywords: coenzyme A biosynthesis; transferase

Query Match 68.5%; Score 923.5; DB 2; Length 267;  
 Best Local Similarity 68.2%; Pred. No. 4.5e-65;  
 Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;

QY 1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLMTVQGHSTLPV 60  
 DB 3 LKQITISLRQWLKANKKFAITAYDASFAQLFAEQGPVMLVGDGLMTVQGHSTLPV 62

QY 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPQAFENATVVRAGANNVKIEGGWLV 119  
 DB 63 SVEDIAHTKSVRRGAPNRLMLADLPMSYATPQAFENATVVRAGANNVKIEGGWLV 122

QY 120 VETVQMLTERAVPVCCHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 179  
 DB 123 FEIVQRLTERSVPVAGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLVL 182

QY 180 ECVPELAKRTEALAIPIVIGAGNVTGQILVMDAFGITGGHIPKPAKFLAETGD 239  
 DB 183 LECIPESLAEQITTKTISPTIGAGKHDTGQILVMDAFGITGGHIPKPAKFLAETGD 242

QY 240 IRAAVRQYMAEVESGVYPGEHSF 263  
 DB 243 IRTAQRVIEVEQGLYPAEHSF 266

RESULT 8  
B84953  
3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) panB [imported] - Buchnera  
C:Species: Buchnera sp.  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: B84953  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: B84953  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-263 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: panB; BU197  
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase  
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 61.5%; Score 830; DB 2; Length 263;  
Best Local Similarity 56.7%; Pred. No. 9.3e-58;

Matches 149; Conservative 59; Mismatches 55; Indels 0; Gaps 0;

QY 1 MKPTTISLQKQKODKRFATITAYDSFAKLFADEGLNVLVGLSDSLGTMVQGHDSITLPV 60  
Db 1 MESITISLQKWKINKKFAITADFSRLEFNSGIPVLIGDSLGMTVQGHDSITLPV 60  
QY 61 TVADIYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVNRAGANMVKIEGGEWLV 120  
Db 61 KIEDIYHTKAVRKGAPNTFLISDLPFMSYVDTKQALKNTAKIIRSGANMVKIEGGEWLI 120  
QY 121 ETVQMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQALLVLECV 180  
Db 121 EIIRLSRLILICDHIGLIPQSHYLGKVGKGRKENDANKLIDEALLLESGINLLIL 180  
QY 181 ECVPELAKRITTEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240  
Db 181 ECIPEKLAKKITESLIFVIGSGKNTDQGLVMDHLLGITEGKTPSFKNFLSDDSI 240  
QY 241 RAAVRQYMAEVESGVYPGEHSF 263  
Db 241 QKAIQKIYIEVHSIYPSKGSF 263

RESULT 9  
E81874  
Probable 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) NMA1088 [imported]  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: E81874  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: E81874  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-263 <PAR>  
A:Cross-references: GB:AL157959; NID:g7379742; PIDN:CAN84351.1; PID:g737978  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: panB; NMA1088  
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase  
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 53.8%; Score 726; DB 2; Length 263;  
Best Local Similarity 55.4%; Pred. No. 1.3e-49;

Matches 144; Conservative 43; Mismatches 71; Indels 2; Gaps 2;

QY 5 TISLLQKQKODKRFATITAYDSFAKLFADEGLNVLVGLSDSLGTMVQGHDSITLPVTVD 64  
Db 3 TVNTLQKMKAAAGEKIAMLTAAYESSFAALMDDAGVDVLVGLSLGMAVQGRQSTLPVSLRD 62  
QY 65 IAYHTAAVRGAPNCLLLADLPFMAY-ATPEQAFENAAATVNRAGANMVKIEGGEWLVETV 123  
Db 63 MCHYTECVARGAKNAMIVSDLPFGAYQQSKQEQAFAAAELMAAGAHMVKIEGGEWMAETT 122  
QY 124 QMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQALLVLECV 183  
Db 123 EFLQMRGIPVCAHIGLTPQSVFAFGYKVGQGRGKA-QALLNDKAKHDDAGAAVVLMECV 181  
QY 184 PVELAKRITTEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKFAKNFLAETGDIRAA 243  
Db 182 PAELAKKVTESVSCPTIGIGAGVDCDQGLVMDHMLGIFPGKTAKEFVKNFMQGSSTQAA 241  
QY 244 VRQYMAEVESGVYPGEHSF 263  
Db 242 VRAYVAEVKAKTFPAAEHIF 261

RESULT 10  
F81148

3-methyl-2-oxobutanate hydroxymethyltransferase NMB0870 [imported] - Neisseria meningi  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: F81148  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.  
Hickey, E.K.; Haff, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.  
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masighani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: F81148  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-263 <TET>  
A:Cross-references: GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF41281.1; PID:g72261  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0870  
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 52.5%; Score 708; DB 2; Length 263;  
Best Local Similarity 54.2%; Pred. No. 3.3e-48;

Matches 141; Conservative 43; Mismatches 74; Indels 2; Gaps 2;

QY 5 TISLLQKQKODKRFATITAYDSFAKLFADEGLNVLVGLSDSLGTMVQGHDSITLPVTVD 64  
Db 3 TVNTLQKMKAAAGEKIAMLTAAYESSFAALMDDAGVEMLLVGLSLGMAVQGRKSTLPVSLRD 62  
QY 65 IAYHTAAVRGAPNCLLLADLPFMAY-ATPEQAFENAAATVNRAGANMVKIEGGEWLVETV 123  
Db 63 MCHYTECVARGAKNAMIVSDLPFGAYQQSKQEQAFAAAELMAAGAHMVKIEGGEWMAETT 122  
QY 124 QMLTERAVPVCGHLGTLTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQALLVLECV 183  
Db 123 EFLQMRGIPVCAHIGLTPQSVFAFGYKVGQGRGKA-QALLNDKAKHDDAGAAVVLMECV 181  
QY 184 PVELAKRITTEALAIPIVIGAGNVTDGQILVMDHAFGITGGHIPKFAKNFLAETGDIRAA 243  
Db 182 LAELAKKVTETVSCPTIGIGAGVDCDQGLVMDHMLGIFPGKTAKEFVKNFMQGHDSVQAA 241  
QY 244 VRQYMAEVESGVYPGEHSF 263  
Db 242 VRAYVAEVKAKTFPAAEHIF 261

RESULT 11  
E82832

3-methyl-2-oxobutanate hydroxymethyltransferase XF0229 [imported] - Xylella fastidiosa

Species: *Xylella fastidiosa*  
Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
Accession: E82832  
Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
Reference number: A82151; MUID:20365717; PMID:10910347  
Note: for a complete list of authors see reference number A59328 below  
Accession: E82832  
Status: preliminary  
Molecule type: DNA  
Residues: 1-246 <SIM>  
Cross-references: GB:AE003876; GB:AE003849; NID:g9105031; PIDN:AAF83042.1; GSPDB:GN001  
Experimental notes: strain 9a5C  
Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Alvarado, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.; Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm, D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, M.A.; Madeira, A.M.B.N.; Madeiral, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Nunes, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracosta, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Santos, L.R.; de Sa, R.G.; de Sa, R.G.; Santelli, R.V.; Sawasaki, A.; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, I.; Tshukano, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zerbini, A.  
Reference number: A59328  
Contents: annotation  
Genetics:  
Gene: XF0229  
Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase  
Query Match 50.9%; Score 686.5; DB 2; Length 246;  
Best Local Similarity 55.1%; Pred. No. 1.5e-46;  
Matches 134; Conservative 37; Mismatches 71; Indels 1; Gaps 1;  
y 22 ITAYDYSFAKLFADGELNVMVLGDSLGMTVQGHSDTLPTVTADIAIYHTAAVRGAPNCLL 81  
b 2 LTAYDAGFARILDANGVDVLVLGDSLSGMVVGHDSTLFPVSVDHVMYHTACVARGVQAML 61  
y 82 LADLPFMAYATPEQAFENATWAGANNMKTGGEWLVEITVQMLTERAVPVCGHLGLTP 141  
b 62 VVDLPFQADSPERALEATPLLRVGAQMIKTEGAGHKLEVISYLVEREIPVCSHLGLTP 121  
y 142 QSVNIIFGYXVQGRGDEAGDQLSDALAEAGALLVLECPVVELAKRITTEALAEIVIG 201  
b 122 QSVLRFGYXVQGRGEEAGGRURAEARAAREAGATLLLELCEVPSQLAAITTDVSVFTIG 181  
y 202 IGAGNVTGCGIILVHDAFGLTGGH-IPKPAKNFLAETGDIIDRAAVROYWAEVSSGVPEEE 260  
b 182 IGAGAGCGGQVLVHLHLLGLDLSHPKPEVKDFLAGGSGVAGAVRANAVRDGSPFDVE 241  
y 261 HSF 263  
b 242 HTY 244  
RESULT 12  
83055  
-methyl-2-oxobutanoate hydroxymethyltransferase PA4729 [imported] - Pseudomonas aeruginosa  
Species: Pseudomonas aeruginosa  
Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
Accession: F83055  
Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brumman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
ature 406, 959-964, 2000  
Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.  
Reference number: A82950; MUID:20437337; PMID:10984043  
Accession: F83055  
Status: preliminary  
Molecule type: DNA  
Residues: 1-266 <STO>

A;Cross-references: GB:AE004866; GB:AE004091; NID:g9950982; PIDN:AAG08115.1; GSPDB:GN001;  
A;Experimental source: strain PAO1  
C;Genetics:  
A;Gene: PA4729  
C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 50.8%; Score 685.5; DB 2; Length 266;  
Best Local Similarity 50.9%; Pred. No. 2e-46; Mismatches 82; Indels 1; Gaps 1;  
Matches 135; Conservative 47;

Cy 1 MKPTTISLLQKYKDKRRPATTITAYDYSFAKLFADEGLNNVLMVGDSLGMTVQGHDSTLPV 60  
Db :  
1 MPDVLTTLTLOGLKQSKEKIAMLTCTYDAIFAHQTASQAGVDVLLVGDLSLGMVLQGHDTLPV 60  
Cy 61 TVADIAHTAAVRGAPNCILLADLPFWAYATPEQA FENAATVMRAGANNVKIEGGWLV 120  
Db :  
61 SNEEMHYATACVRKGNGSLIVTDLAFESSHSVAOTLADAVRLAQAGAHHMVKLEGGVWL 120  
Cy 121 ETVOMLTERAVPCVCHGLGTPOSVNI FG YKVQGRGEAGDQLLSDALALEAAGAILLV 180  
Db :  
121 EPIARLAQMGPVCACHGLGTPOAVNLFGGVQGRQETQARQLRADAI LEQAANMLL 180  
Cy 181 ECYPVELAKRITEALAI PVIGAGNVTDGOILVMHDAFGIT-GSHIPKPAKNFLAETGD 239  
Db :  
181 ECVPSVLAEIITQAVKIPVIGIGAGAADGOVNMHDLGLSLTGSRSPKFVKDFMQGES 240  
Cy 240 IRAAVRYMAEVESGYVPCEEHSFH 264  
Db :  
241 IPAATAAYRAVKDVSPFAAEHGHN 265

RESULT 13  
G83860  
ketopantoate hydroxymethyltransferase panB [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: G83860  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai,  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
its relatives.  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: G83860  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-279 <STO>  
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05406.1; GSPDB:GN001;  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: panB  
C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 46.5%; Score 627; DB 2; Length 279;  
Best Local Similarity 46.7%; Pred. No. 7.9e-42;  
Matches 122; Conservative 59; Mismatches 78; Indels 2; Gaps 2;

Cy 5 TTSLQKYKDYKKRPATTITAYDYSFAKLFADEGLNNVLMVGDSLGMTVQGHDSTLPVTAD 64  
Db :  
3 TTA SPKKMKQQCKEIKIAMTVAPSARLVEDADMVILVGDLSLGMVLYGYDSTTFVTLD 62  
Cy 65 IAVHTAAVRGAPNCILLADLPFWAY-ATPEQA FENAATVMR-AGANNVKIEGGWLVET 122  
Db :  
63 MUHHTAVRGAKNTFTVDPYLTYHGSFNETHVGA RLMOEA GA DLKLEGNDIIDT 122  
Cy 123 VQMLTERAVPCVCHGLGTPOSVNI FG YKVQGRGEAGDQLLSDALALEAAGAILLVLEC 182  
Db :  
123 IERLTLAGVPI VAHLGLTPQNVAVEGGYRVQAKDKSAKQLLADAKAVEAAGAFALVLEC 182  
Cy 183 VPVELAKRITEALAI PVIGAGNVTDGOILVMHDAFGITCGHIPKPAKNFLAETGDIRA 242  
Db :  
183 VFQVATQISELTIPTVIGAGCDGQVLYTHDIVGYGAGHVPSFKOVNITPFEE 242  
Cy 243 AVRQYMAEVESGYVPCEEHSF 263  
Db :

Db 243 AMKQYVQEVKAGTFPDKDHAF 263

RESULT 14

G69671

kecopantoate hydroxymethyltransferase panB - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000

C;Accession: G69671

R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni, A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, C.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, A.; Authors: M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69671

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-277 <KUN>

A;Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14159.1; PID:g2634661

A;Experimental source: strain 168

C;Genetics:

A;Gene: panB

C;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 46.1%; Score 622; DB 2; Length 277;

Best Local Similarity 47.8%; Pred. No. 1.9e-41;

Matches 122; Conservative 50; Mismatches 81; Indels 2; Gaps 2;

QY 11 KYQDKKRPATITAYDYSFAKLFADEGLNVMVLGDSLGMTVOGHDSTLPTVTADIAVHTA 70

Db 9 KMKSEBPIVMTAYDYPAAKLAQAGVDMILVGLSGVGLDSTVGVTVADMIHHTK 68

QY 71 AVERGAPNCLLDLADLPFVAY-ATPQAFENAAATVNR-AGANVMKIEGGEWLVTQVQLTE 128

Db 69 AVKRGAPNFFIVTDMFPFSYHLSKEDTLKNAAIQVESGADALKLEGEGVFESIRALT 128

QY 129 RAVFVCGHLGLTPQSVNIFGGYKVGGRDEAGDQLSDALALEAAGQLLVLECVVELA 188

Db 129 GGIPVSHGLTPQSGVGLGKVGQKQEQSAKLIEDSIKCEBAGMLVLECVPAELT 188

QY 189 KRITALEAIPVIGIGAGNVTGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAAVRQYM 248

Db 189 AKIAETLSIPVIGIGAGVKAQGVLYVYHDIIGHGVERTPKVQYTRIDETIETAISSYV 248

QY 249 AEVSGVYPGEEHSF 263

Db 249 QDVRHRAFPPEQKHSF 263

RESULT 15

G72216

3-methyl-2-oxobutanate hydroxymethyltransferase - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C;Accession: G72216

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: G72216

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-270 <ARN>

A;Cross-references: GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AAD36793.1; PID:g49823

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1728

C;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 45.4%; Score 612; DB 2; Length 270;

Best Local Similarity 47.5%; Pred. No. 1.1e-40;

Matches 123; Conservative 52; Mismatches 82; Indels 2; Gaps 2;

QY 6 ISLLQYKQDKRPATITAYDYSFAKLFADEGLNVMVLGDSLGMTVOGHDSTLPTVTADI 65

Db 3 VEKUKQVK-GKEKIVMTATDAPASARIARDAGIDVILVGLSGLNNVLYGENTIPVTMEEM 61

QY 66 AYHTAAVRRGAPNCLLDLADLPFVAYATP-EQAFENAAATVNRAGANVMKIEGGEWLVTQV 124

Db 62 LIHVAAVKRGAPDAFIVADNPFLSYQTSVEKAVENAGKFLKVGANAVKIEGGEFGLVQ 121

QY 125 MLTERAVPVCCHGLITPQSVNIFGGYKVGGRDEAGDQLSDALALEAAGQLLVLECV 184

Db 122 KLVESGIPVMGHIGLTPQVNRFGYKVGQKTEKNREYLLRSARELEKRGAFVILELVV 181

QY 185 VELAKRITEALAIPIVIGIGAGNVTGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAAV 244

Db 182 EEVAKETESVSIPTIGIGSGRFGDQGVLYVHDLGLNPDFAFPFSKKNVLYEVILKAL 241

QY 245 RQYMAEVSGVYPGEEHSF 263

Db 242 QEPREVKKGLFPTEHSF 260

Search completed: July 29, 2004, 10:34:57

Job time : 16 secs

GenCore version 5.1.6  
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M protein - protein search, using sw model

run on: July 29, 2004, 10:32:16 ; Search time 19 seconds  
(without alignments)  
717,329 Million cell updates/sec

Title: US-09-820-745-7  
Perfect score: 1349  
Sequence: 1 MKPTTISLLQKQDKKREFA.....ROYMAEVESGVYPGEHSFH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/POCUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1204.5	89.3	270	4	US-09-489-039A-12261
2	968.5	71.8	281	4	US-09-543-681A-6233
3	726	53.8	284	4	US-09-328-352-7946
4	689	51.1	284	4	US-09-540-236-1925
5	686.5	50.9	303	4	US-09-252-991A-26922
6	598.5	44.4	275	4	US-09-107-532A-4013
7	598.5	44.4	275	4	US-09-134-000C-6528
8	527.5	39.1	271	3	US-09-318-794A-2
9	527.5	39.1	271	3	US-09-318-793A-4
10	522.5	38.7	274	4	US-09-134-001C-4406
11	520.5	38.6	274	4	US-08-956-171B-5243
12	482	35.7	375	4	US-09-903-814A-2
13	424	31.4	227	4	US-09-252-991A-25961
14	114	8.5	531	4	US-09-252-991A-31109
15	97.5	7.2	1621	1	US-08-242-677-2
16	96	7.1	500	4	US-09-328-352-6757
17	92.5	6.9	959	4	US-09-252-991A-21747
18	92	6.8	403	4	US-09-489-039A-11881
19	91.5	6.8	582	4	US-09-252-991A-217626
20	90	6.7	1051	4	US-09-252-991A-19145
21	89.5	6.6	343	4	US-09-328-352-5814
22	89	6.6	484	4	US-09-543-681A-4699
23	88.5	6.6	1019	4	US-09-252-991A-24417
24	88.5	6.6	1026	1	US-08-194-290-7
25	88.5	6.6	1026	2	US-08-614-377A-7
26	88.5	6.6	1026	3	US-09-142-648B-7
27	88	6.5	654	4	US-09-134-000C-6616

ALIGNMENTS

RESULT 1

US-09-489-039A-12261

; Sequence 12261, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 12261

; LENGTH: 270

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12261

Query Match 89.3%; Score 1204.5; DB 4; Length 270;

Best Local Similarity 89.0%; Pred. No. 8.4e-129;

Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MKPTTISLLQKQDKKREFAITAYDYSFAKLFADEGLNVLVGLVSGMTVQGHDSITLTPV 60

Db 8 MKPTTIALQKCKQKRRFATITAYDHSFAKLFADEGINVLVGLVSGMTVQGHDSITLTPV 67

Qy 61 TVADIAYHTAAVRRGAPNCLLLADJPFMAIATPEQAFENAAATVMAGANWVKIEGEMIV 120

Db 68 TVEDIAVHTAVRRGAPNSLLLLADJPFMAIATPECTFANAATVMAGANWVKIEGAWLA 127

Qy 121 ETVQMLTERAPVCGHGLTTPQSVNIFGKYKQGGDAGDGLLSDALAEAGALLVL 180

Db 128 DTVRMIAERAPVCGHGLTTPQSVNIFGKYKQGGD-AAQTLFEDALAEAGALLVL 186

Qy 181 ECVPELAKRITTEALAIPIVIGICAGNVTDQGLVNMHDAFGITGGHIPKFAKNFLAETGDI 240

Db 187 ECVPELAKRITDALTIPVIGICAGNVTDQGLVNMHDAFGITGGHIPKFAKNFLAEGDI 246

Qy 241 RAAVRQYIAEVESGVYPGEHSFH 264

Db 247 RAAVRQYIAEVESGVYPGEHSFH 270

RESULT 2

US-09-543-681A-6233

; Sequence 6233, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 ; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709,1002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543,681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 6233  
 ; LENGTH: 281  
 ; TYPE: PRT  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-6233

Query Match 71.8%; Score 968.5; DB 4; Length 281;  
 Best Local Similarity 70.8%; Pred. No. 6.9e-102;  
 Matches 187; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 1 MKPTTSLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 60  
 DB 19 MKPVTLSLTRYKQEKKFRATITAYDASFAFLFANEGIPAMLLIGDSLGMTLQGHDSLTPV 78  
 QY 61 TVADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAVMRAGANVMKIEGGSWLV 120  
 DB 79 TVEQIAHYHTRCVRGAPNAFLIADPFMSYSTPEQACLNAAIIMQAGANVMKIEGGSWLI 138  
 QY 121 ETVMQLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVL 180  
 DB 139 PTVKMLTERAVPVCIHGLTPQSVNVFVGGYKVGQREAAEQKQADAMALEAAGALLVL 198  
 QY 181 ECVPELAKRTEALAIPIVIGAGNVTDGQILVMDHAFGTTGGHIPKAKNFLEAGDI 240  
 DB 199 ECVFVSVAITIGSLNIPVIGAGNVTDGQILVMDHLLGT-PNAPKFSKNFLQEAGSL 257  
 QY 241 RAAVROYMAEVESGVYPGEHSF 264  
 DB 258 PEAVRLYVQVQKLPQEQHSEFN 281

RESULT 3  
 US-09-328-352-7946  
 ; Sequence 7946, Application US/09328352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: GTC99-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 7946  
 ; LENGTH: 284  
 ; TYPE: PRT  
 ; ORGANISM: Acinetobacter baumannii  
 US-09-328-352-7946

Query Match 53.8%; Score 726; DB 4; Length 284;  
 Best Local Similarity 54.0%; Pred. No. 2.9e-74;  
 Matches 142; Conservative 48; Mismatches 69; Indels 4; Gaps 3;

QY 5 TISLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVTAD 64  
 DB 18 SLSDLKFKAEGRKFSCLTCYDASMAKAMELAIEDTILIGDSLGMATQGRDSTLPVTVD 77  
 QY 65 IAYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAVMRAGANVMKIEGGSWLVETVQ 124  
 DB 78 MAYHTAAVRGQHAHIMTDLFPNSYATINDALQNAKVMQAGQMIEGGAWLSETVQ 137  
 QY 125 MLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVLECPV 184  
 DB 138 VLTFNGVPCVHLGTPQSVHFGYKVLQARTREAADQLIADCTAVVEAGAVALLECPV 197

QY 185 VELAKRITEALA-IPVIGAGNVTDGQILVMDHAFGTTGGHIPKAKNFLEA-TGD--I 240  
 DB 198 AOLQGEIAELFPNTFVIGAGNATDQVLVQDMLGTFGRVARTVRNFMKEQSGETAI 257  
 QY 241 RAAVROYMAEVESGVYPGEHSF 263  
 DB 258 LDAFKAFHAAVQDSQSFPAKEHTF 280  
 RESULT 4  
 US-09-540-236-1925  
 ; Sequence 1925, Application US/09540236  
 ; Patent No. 6673910  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT7  
 ; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 2709,2005-001  
 ; CURRENT APPLICATION NUMBER: US/09/540,236  
 ; CURRENT FILING DATE: 2000-04-04  
 ; NUMBER OF SEQ ID NOS: 3840  
 ; SEQ ID NO 1925  
 ; LENGTH: 284  
 ; TYPE: PRT  
 ; ORGANISM: M. catarrhalis  
 US-09-540-236-1925

Query Match 51.1%; Score 689; DB 4; Length 284;  
 Best Local Similarity 53.6%; Pred. No. 4.8e-70;  
 Matches 142; Conservative 34; Mismatches 85; Indels 4; Gaps 1;  
 QY 3 PTTTSLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVTV 62  
 DB 20 PITLSTLNKLAEGKTFSCITCEASPAHAMQADITDILIGDSLGMVQGSSTLPVGV 79  
 QY 63 ADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAVMRAGANVMKIEGGWLVET 122  
 DB 80 QDMVYHTQNVVRGNHALILCDLPFMSYATLSDAITSKAVMQAGANVMKIEGSELSDT 139  
 QY 123 VQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVLEEC 182  
 DB 140 VKVLTNNGVPVCGVHLGTPQSVNVFVGGYKVGQKIDQADKLMDCCTAVVNAGASLLLEEC 199  
 QY 183 VPVELAKRITEALAIPVIGAGNVTDGQILVMDHAFGTTGGHIPKAKNFLEA----ETG 238  
 DB 200 VPAPLAKAVTERFDPVPIGAGVDTDQVLVMDHMLGIYTRKPAKFNKFLTDSDSNQTK 259  
 QY 239 DIRAAVROYMAEVESGVYPGEHSF 263  
 DB 260 DIVGAFAKAYHAAVQKRAFPTKQHSF 284

RESULT 5  
 US-09-252-991A-26922  
 ; Sequence 26922, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196,136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 26922  
 ; LENGTH: 303  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa

JS-09-252-991A-26922

Query Match 50.9%; Score 686.5; DB 4; Length 303;  
Best Local Similarity 50.9%; Pred. No. 1e-69;  
Matches 135; Conservative 47; Mismatches 82; Indels 1; Gaps 1;  
Y 1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDSTLPV 60  
b 38 MPDVTLLTLOGLKQSGEKIAMLCYATFAHTASQAGVDVLLVGDLSLGMTVQCHDSTLPV 97  
Y 61 TVADIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANMVKIEGEMLV 120  
b 98 SNEEMAYHTACVRKNGKSLIVTDLPESHSHVAQTLADAVRLMQAGMVKIEGEMLV 157  
Y 121 ETVOMLTERAVPVCGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGAQLVL 180  
b 158 EPIARLAQMGVPVCAHLGLTPQAVNLPGGFKVQGRQETQARQLRADAI ALEAQAAMLL 217  
Y 181 ECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGIT---GGHIPKFAKNFLAETGD 239  
b 218 ECVPSVLAELITQAVKIPVIGIGAGNATDQGLVMDHMLGLSLTGRSPKPFVKDFMQGES 277  
Y 240 IRAAVROQYMAEVESGVYPGEHSFH 264  
b 278 IPAAIAAYVRAVDVSPFAAEHGFN 302

RESULT 6

JS-09-107-532A-4013  
Sequence 4013, Application US/09107532A  
Patent No. 6583275

## GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

## NUMBER OF SEQUENCES: 7310

## CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

## COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

## INFORMATION FOR SEQ ID NO: 4013:

## SEQUENCE CHARACTERISTICS:

LENGTH: 275 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

## FEATURE:

NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...275  
SEQUENCE DESCRIPTION: SEQ ID NO: 4013:  
US-09-107-532A-4013

## Query Match 44.4%; Score 598.5; DB 4; Length 275;

Best Local Similarity 45.5%; Pred. No. 9.4e-60;  
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

Y 1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDST 57  
b 1 MKNTAVT---FKESKLREKLTMLTAYDYSATAIIDEAGINGILVGDLSLGMTVQCHDST 56  
Y 58 LPTVADIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAG-ANMVKIEG 115  
b 57 LSVTMDMIHTTAVTRGAKNTLVADMPFNSTQTSYDVSVDVNVNAGRLIKEGRAQVVKLEG 116  
Y 116 GEWLIVETVQMLTERAVPVCGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGA 175  
b 117 GIEVCDKIEAIVKASIPVMAHIGLTQPSVNAFGGFKVQGRDEAGDQLLSDALALEAAGA 176  
Y 176 QLLVLECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLA 235  
b 177 FAVVLECVPTKLAELISKISIPITIGIGAGAGCDGQILVYQDMLGMYSDFTFKFKVKYAN 236  
Y 236 ETGDIRAAVRQYMAEVESGVYPGEHSF 263  
b 237 LSBE MNKFTKYLEEVKDGVPFGPEHGF 264

RESULT 7

US-09-134-000C-6528  
Sequence 6528, Application US/09134000C  
Patent No. 8617156

## GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

## FILE REFERENCE: 032796-032

## CURRENT APPLICATION NUMBER: US/09/134,000C

## CURRENT FILING DATE: 1998-08-13

## PRIOR APPLICATION NUMBER: US 60/055,778

## PRIOR FILING DATE: 1997-08-15

## NUMBER OF SEQ ID NOS: 6812

## SOFTWARE: PatentIn version 3.1

## SEQ ID NO 6528

## LENGTH: 275

## TYPE: PRT

## ORGANISM: Enterococcus faecalis

US-09-134-000C-6528

## Query Match 44.4%; Score 598.5; DB 4; Length 275;

Best Local Similarity 45.5%; Pred. No. 9.4e-60;  
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

Y 1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDST 57  
b 1 MKNTAVT---FKESKLREKLTMLTAYDYSATAIIDEAGINGILVGDLSLGMTVQCHDST 56  
Y 58 LPTVADIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAG-ANMVKIEG 115  
b 57 LSVTMDMIHTTAVTRGAKNTLVADMPFNSTQTSYDVSVDVNVNAGRLIKEGRAQVVKLEG 116  
Y 116 GEWLIVETVQMLTERAVPVCGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGA 175  
b 117 GIEVCDKIEAIVKASIPVMAHIGLTQPSVNAFGGFKVQGRDEAGDQLLSDALALEAAGA 176  
Y 176 QLLVLECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLA 235  
b 177 FAVVLECVPTKLAELISKISIPITIGIGAGAGCDGQILVYQDMLGMYSDFTFKFKVKYAN 236  
Y 236 ETGDIRAAVRQYMAEVESGVYPGEHSF 263

Db 237 LSENNKAFKXIEVKDGVFGPEHGF 264

# RESULT 8

US-09-318-794A-2

; Sequence 2, Application US/09318794A

; Patent No. 6177264

; GENERAL INFORMATION:

; APPLICANT: DEGUSSA AKTIENGESSELLSCHAFT

; TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC

; FILE REFERENCE: ACID USING CORYNEFORM BACTERIA

; CURRENT FILING DATE: 1999-05-26

; CURRENT APPLICATION NUMBER: US/09/318,794A

; PRIOR FILING DATE: 1999-05-26

; PRIOR APPLICATION NUMBER: DE 198 55 312.9

; PRIOR FILING DATE: 1998-12-01

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 271

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-318-794A-2

Query Match 39.1%; Score 527.5; DB 3; Length 271;

Best Local Similarity 43.1%; Pred. No. 1.1e-51;

Matches 109; Conservative 52; Mismatches 89; Indels 3; Gaps 3;

QY 13 KODKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSITLPTVTADIAHTAAV 72

DB 20 KNGOKSVLTSYDALSARIFDEAGVDMLLVGLDGSAAVVLGRDTTILSITIDEMIVLAKAV 79

QY 73 RRGAPNCLLLADLPFMAY-ATPEQAFENAAVTMR-AGANVMYKIEGGEWLVETVQMLTERA 130

DB 80 TIATKRALVVDLPFGTYEVSQAVESAIRVMRETGAAGVAVKIEGVEIAQTIRRIVDAG 139

QY 131 VPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVLECVPEVELAKR 190

DB 140 IPVVGHIPTYQSEHSLGHVVGQGRGASSG-KLIADARALEQAGAFVVLVEMVPAEARE 198

QY 191 ITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDIRAAVROYMAE 250

DB 199 VTEDLSITTIIGAGNGTDGQVLVWQDAFGLNKGKPRFVREYATILGDSLHDAQAAYIAD 258

QY 251 VESGVYPGEHSF 263

DB 259 IHAGTFPGEAESF 271

# RESULT 9

US-09-318-793A-4

; Sequence 4, Application US/09318793A

; Patent No. 6184007

; GENERAL INFORMATION:

; APPLICANT: Dusch, Nicole

; APPLICANT: Kalinowski, Jörn

; APPLICANT: Puhler, Alfred

; TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC

; FILE REFERENCE: ACID BY ENHANCEMENT OF THE PAND GENE IN MICROORGANISMS

; CURRENT FILING DATE: 1999-05-26

; CURRENT APPLICATION NUMBER: US/09/318,793A

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 271

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-318-793A-4

Query Match

Best Local Similarity 39.1%; Score 527.5; DB 3; Length 271;

Matches 109; Conservative 52; Mismatches 89; Indels 3; Gaps 3;

QY 13 KODKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSITLPTVTADIAHTAAV 72

DB 20 KNGOKSVLTSYDALSARIFDEAGVDMLLVGLDGSAAVVLGRDTTILSITIDEMIVLAKAV 79

QY 73 RRGAPNCLLLADLPFMAY-ATPEQAFENAAVTMR-AGANVMYKIEGGEWLVETVQMLTERA 130

DB 80 TIATKRALVVDLPFGTYEVSQAVESAIRVMRETGAAGVAVKIEGVEIAQTIRRIVDAG 139

QY 131 VPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVLECVPEVELAKR 190

DB 140 IPVVGHIPTYQSEHSLGHVVGQGRGASSG-KLIADARALEQAGAFVVLVEMVPAEARE 198

QY 191 ITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDIRAAVROYMAE 250

DB 199 VTEDLSITTIIGAGNGTDGQVLVWQDAFGLNKGKPRFVREYATILGDSLHDAQAAYIAD 258

QY 251 VESGVYPGEHSF 263

DB 259 IHAGTFPGEAESF 271

# RESULT 10

US-09-134-001C-4406

; Sequence 406, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4406

; LENGTH: 274

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4406

Query Match 38.7%; Score 522.5; DB 4; Length 274;

Best Local Similarity 43.7%; Pred. No. 4.2e-51;

Matches 114; Conservative 47; Mismatches 95; Indels 5; Gaps 5;

QY 5 TISLIQKYKQDKRFAITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSITLPTVTAD 64

DB 5 TLNHLNKMKASQKISMTVAYDYSFAKQAQQAQAEIDMLVGLDGLMTVGLYDSTVQVTLND 64

QY 65 IAYHTAAVRGAPNCLLLADLPFMAYA-TPEQAFENAAVT-MRAGANVMYKIEGGEWLVET 122

DB 65 MIHKGAVKRGASDTFIVDMPIGTGVLSDDEEDLKNALKLYQNTNANAVKVEGAH-LTSP 123

QY 123 VQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVLEEC 182

DB 124 IQKATKMGIPVVLGHLTPQSVGM-CYKLGQDTKTAAMQLIKDAKAMETAGAVVLVLEA 182

QY 183 VPVELAKRITETALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDIRA 242

DB 183 IPSDLAREISQQLTIPVIGIGAGKDTGQVLVYHDMNLNYGVDRHAKFVKQADFSSGI-D 241

QY 243 AVROYMAEVESGVYPGEHSF 263

DB 242 GLRQINEEVKAGTFPSENHTY 262

# RESULT 11

US-08-956-171E-5243

; Sequence 5243, Application US/08956171E

; Patent No. 6593114



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US-09-903-814A-2
; Sequence 2, Application US/09903814A
; Patent No. 6680428
; GENERAL INFORMATION:
; APPLICANT: Falco, Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes
; FILE REFERENCE: BB1179 USDIV
; CURRENT APPLICATION NUMBER: US/09/903,814A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/092,869
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: US 09/351,703
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Zea mays
US-09-903-814A-2

Query Match          35.7%; Score 482; DB 4; Length 375;
Best Local Similarity 40.1%; Pred.No. 2.8e-46;
Matches 107; Conservative 49; Mismatches 101; Indels 10; Gaps 6;

Qy      5 TISLLQKYQDKRRFATITAYDYSFAKLFEADBSGLNVMYVGDLSGMTVGQHDSTLPVTVD 64
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      66 TVTTLRGKRRGEPIWTWTDYPSAVHVSDSAGIDVCLVGDAAVMVHGHTTLPITLDI 125

Qy      65 IAVHTAAVRGAPNCILLADLPFMAY-ATPEQAFFENAATVMR-AGANMVKIEGG-EWLVE 121
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      126 MLEHCRVARGARPRPLVGLDFPGCVESAAQAQVDSAVRVLKEGGMDAKLEGGAFSRIT 185

Qy      122 TVQMILTERAVPVCGHLGLTPQSVNIFGGYKVQGRDEAGDQLLSDALALEAAGAQLLVLE 181
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      186 AKAAIVEAGIYAVMGHVLTPQAISVLGGRPQCKTVDSAIKVVETALALQEAGCFSWILE 245

Qy      182 CVPVELAKRITEALATPVIGIGAGNVTDGQILVMHDAFGIT----GGHIPKFKNFLAE 236
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      246 CVPAVVAATAASALKPTTGIGAGPCSCQVLYHDLMLQHPHHIAKTPECKQF-GN 304

Qy      237 TGD-IRAAVRQYMAEVESGVYPGEHS 262
       : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      305 VGDVINKALSEYKQVEAQAFPGPSHT 331

RESULT 13
US-09-252-991A-25961
; Sequence 25961, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25961
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25961

```

### Query Match

31.4%; Score 424; DB 4; Length 227;

Best Local Similarity 42.2%; Pred. No. 5.3e-40;  
Matches 87; Conservative 39; Mismatches 78; Indels 2; Gaps 2;  
QY 60 VTVDATYHTAAVRRGAPNCLLLADLPFMAV-ATPEQAFENAAVTMR-AGANVMKIEGGE 117  
Db 18 VSLSEMVATLWVRGSRACVADLPFASVQESPRQAFRNAARLADSGAQAQVLSGGE 77  
QY 118 WLVTETVOMLTERAVPCYGHGLTPTQSVNIFGQYKVGGRDEAGDQLLSDALALEAQAQL 177  
Db 78 EMEETVDFLVRGIPVLAIHGLMPQVNMAGGFKAGRDPSAERVRDGLAMQGGAGA 137  
QY 178 LVLECVVSELAKRITALEAIPVIGIGAGNVTDGQILVMHDAFGITGGHIPKFAKNFLAET 237  
Db 138 VVIEGVGEPLARLSBELAIPICIGIGASGACDQVLSVSDLLGSGEQVPRFERYARLD 197  
QY 238 GDRAARVQYMAEVESGVYPGEHSF 263  
Db 198 REIDEAARRFAEDVRERPFERHCF 223  
RESULT 14  
US-09-252-991A-31109  
; Sequence 31109, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31109  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31109  
Query Match 8.5%; Score 114; DB 4; Length 531;  
Best Local Similarity 27.7%; Pred. No. 0.00041;  
Matches 81; Conservative 28; Mismatches 99; Indels 84; Gaps 17;  
QY 37 GLNVMVGLSGMTVQGHDSLTPVTVDIAYHTAAVRRGA---PNCLLIADLPFMA--- 89  
Db 140 GLQV-----EIGHAVDGRVPTAGAAVGDALQAAAVLRQGAARQAQAFADQVFLARGA 194  
QY 90 ---YATPRQA---FENATVNRAGANVMVKI-----EGGEWLVTETV-----QMLTER 129  
Db 195 AVVVLAVAGQLLGDREVEADVEQAGVLVATEVLGLDEAGVGVALVAEDAIQIQRVADR 254  
QY 130 AVPVCGHLGLTQSV-----NIFGQYKVG-----RG-----DEAGQLLSDALALE 171  
Db 255 LVDLDLPHVRHQVQVAAAARGVRRRQQLQGLVGDARRGADQAEALDHFGAALLAGVMVAE 314  
QY 172 AAGAQLLVLECVVSELAKRITALEAIPVIGIGAGNV-----TDGQILVMHDAF 219  
Db 315 TAG--LAVNAVVGSGAGARIDALLVLLVLLGAGVQVVELFLAADFEEYAPVHQALVARHLG 372  
QY 220 GITGHHIPKFAKNFLA--ETGD-----IR-----AAVRQYMAEVESGVYPGE 259  
Db 373 GLIG-----BQFVALGEGGGRVLRRAILRAAACTROSADVEQGV-FGD 416

## RESULT 15

US-08-242-677-2  
; Sequence 2, Application US/08242677  
; Patent No. 5677143  
; GENERAL INFORMATION:  
; APPLICANT: Gaynor, Richard B

APPLICANT: Wu, Poon W.  
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein  
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the  
TITLE OF INVENTION: Treatment of AIDS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/242,677  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mayfield, Denise L.  
REGISTRATION NUMBER: 33,732  
REFERENCE/DOCKET NUMBER: UTSD:401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1621 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-242-677-2  
Query Match 7.2%; Score 97.5; DB 1; Length 1621;  
Best Local Similarity 26.0%; Pred. No. 0.17;  
Matches 56; Conservative 27; Mismatches 91; Indels 41; Gaps 9;  
QY 37 GLNVMVGLSGMTVQGHDSLTPVTVDIAYHTAAVRRGA---PNCLLIADLPFMAVAT 92  
Db 67 GYLVELLSRGRPAGGPDPSLQ-----PRHRRVLRAGAAALRSCVRLAGRPQAAAL 120  
QY 93 PQAFENAAVTNRAGANVMKIEGGEWLVTETVQ-----MLTERAVPVCGHLGLTQSVNIF 147  
Db 121 ABEALRDLLAGWRA-----PGNEAAVEVLAAVGCPLRPREDGPIILLERVAGCTAVALG 173  
QY 148 GGYKVGQGRDAGDQLLSDALALEAQAQLLVLECVVSELAKRITALEAIPVIGIGAGNV 207  
Db 174 GG---GDGDEAGP--AEDAAALVAGRLLEVLVQCGGAAL--RAVWGGLAAPGASLGSGRV 226  
QY 208 TDGQILVMHDAFGITGGHIPKFAKNFLAETGDIRA 242  
Db 227 EE-KLLV-----LSALAEKLLPEPGDRA 249  
Search completed: July 29, 2004, 10:35:28  
Job time : 20 secs